



PD 20-MAY-1999.  
 XX  
 PF 09-OCT-1998; 98MO-IB01665.  
 XX  
 PR 01-SEP-1998; 98GB-0019016.  
 PR 06-NOV-1997; 97GB-0023516.  
 PR 14-NOV-1997; 97GB-0024190.  
 PR 18-NOV-1997; 97GB-0024386.  
 PR 27-NOV-1997; 97GB-0025158.  
 PR 10-DEC-1997; 97GB-0026147.  
 PR 14-JAN-1998; 98GB-0000759.  
 XX  
 PA (CHIR-) CHIRON SPA.

PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
 XX WPI: 1999-327407/27.  
 DR N-PSDB; AAZ12174.  
 XX

Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for  
 PT diagnosis, treatment and prevention of infection  
 XX

PS Claim 4; Page 277; 524pp; English.

XX Amino acid sequences AAY38499-V38944 represent *Neisseria meningitidis*  
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open  
 CC reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins,  
 CC their fragments, their nucleic acids and antibodies are used for  
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*  
 CC infections, such as meningitis, septicemia and gonorrhea. Both  
 CC organisms are closely related. Fragments of the nucleic acids  
 CC are useful as hybridisation probes and antisense reagents.  
 XX

SQ Sequence 556 AA:

alignment\_scores:      Quality: 2202.00      Length: 560  
                          Ratio: 4.597              Gaps: 8  
                          Percent Similarity: 85.536      Percent Identity: 77.679

alignment\_block:

US-09-303-518d-463 x AAY38731 ..

Align seg 1/1 to: AAY38731 from: 1 to: 556

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1 TTGGGCAATTCGCCGAAATATCCCTTATTCGTCATCTGCGACATG 50
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1 LeuGlyIleSerArgLysIleSerLeuIleLeuSerIleLeuAlaVal 17
51 CCGCGCATGCATGCACAGCCCTCAGATTGGCAAGCATCCCTTATCC 100
  |||||
17 sleuPromethiAlaHisAlaSerAspLeuAlaAsnAspSerPheIle 34
101 GCGAGGTTCCGACGCTCAGCATTTGGAACCGGCGGAATTCACACCT 150
  |||||
34 rglInValIleuAspArgGlnHisPheGluProSprLysTyrHisIleu 50
151 TTGGGAGAGGAGGGGAGCTTGGCCNAGCGAAGCGCCATGATGGATGG 200
  |||||
51 PheGlySerArgGlyLysIleuAlaGluArgSerGlyHisIleIleu 67
201 AAACATACAAAGCCATCAGTTGGGCGACCTGATGATTCACAGCGCGCG 250
  |||||
67 yAsnIleGlnSerHisGlnIleuGlyAsnLeuPheIleGlnAlaIle 84
251 TTCAAGGAATATCGGCTACATTCGCTTTTCGATCAGGCGCAAA 300
  |||||
84 IeLysGlyAsnIleGlyTyrIleValArgPheSerAspHisGlyHisGlu 100
301 TTCCATTCGCGCTTGCACAACCATGCTCACAATTCGATTCGAGCGAAC 350
  |||||
101 ValHisSerProPheAspAsnHisAlaSerHisSerAspSerPheIle 117

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351 GCGTAGTCCCGCTTGACGATTCAGCCTTACCGCATTCATTCGACGGAT 400
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117 aGlySerProValAspGlyPheSerLeuTyrArgIleHisTrpAspGly 134
401 ACGAACACCATCCCGCCGACGGCTATGACGGGCGCCACAGGGCGGGCTAT 450
  |||||
134 yGlnHisHisProAlaAspGlyTyrAspGlyProGlnGlyGlyTyr 150
451 CCCGCTCCCAAAAGCGCGAGGGATATATACAGCTACGACATAAAGCGGT 500
  |||||
151 ProAlaProLysGlyAlaArgAspIleTyrSerTyrAspIleLysGlyVa 167
501 TCGCCAAATATCCGCTCAACCTGACGAGCAACCGGACCGGACACAC 550
  |||||
167 lAlaGlnAsnIleArgLeuAsnLeuThrAspAsnArgSerThrGlyIle 184
551 GCGTTGGCGACCGTTCCACAATGCCGCGCTATGCTGACGCAAGAGTA 600
  |||||
184 rGlyValAlaSprPheHisAsnThrGlySerMetLeuThrGlnGlyVal 200
601 GCGCAGCATTCAAACGCCCAACCGCATACAGCCCGGAGCTTGACACATC 650
  |||||
201 GlyAspGlyPheLysArgAlaThrArgTyrSerProGluLeuAspArgSe 217
651 GCGCAATGCGCGCGAAGCCTTCAACGCGCATGCAAGATATCGTCAAAA 700
  |||||
217 rGlyAsnAlaAlaGlnAlaPheAsnGlyThrAlaAspIleValLysAsn 234
701 TCATCGCGCGCGCAGAGAAATGTCGGCGCAGCGATCCGTCAGAGGT 750
  |||||
234 lIleGlyAlaAlaGlyIleValGlyAlaGlyAlaAspAlaValGlnGly 250
751 ATACCGAAGGCTCAAAACATTCGTGTCATGACGCGCTTGCTGCTTTC 800
  |||||
251 lIleSerGluGlySerAsnIleAlaValMetHisGlyLeuGlyLeuLeuSe 267
801 CACCGAAACAAAGATGGCGGCATCAACGATTTGGCAGATTTGGCGCAAC 850
  |||||
267 rThrGlnAsnLysMetAlaArgIleAsnAspLeuAlaAspMetAlaGln 284
851 TCAAAAGACTATGCGCGACGACCATCCGATTTGGCATGCCAAACCC 900
  |||||
284 euLysAspTyrAlaAlaAlaIleArgAspTyrAlaValGlnAsnPro 300
901 AATGCCGCAACAAGCATGGAAGCGGTGACGAAATCTTATGAGCAGCAT 950
  |||||
301 AsnAlaAlaGlnGlyIleGluAlaValSerAsnIlePheThrAlaVal 317
951 CCCCATCAAAAGGATTTGAGCTGTCCGGGGAATAACGCGTTGGCGCGCA 1000
  |||||
317 eProValLysGlyIleGlyAlaValArgGlyLysTyrGlyLeuIleGly 334
1001 TCACGCGCATTCCTGTCAAGCGGTCCGACATGGCGCGGATTCGCTCCG 1050
  |||||
334 lIleThrAlaHisProValLysArgSerGlnMetGlyGluIleAlaLeuPro 350
1051 AAAGGAAATCCGCGCTGACGAGACAATTTGGCATGCGGATCGGCAAA 1100
  |||||
351 LysGlyLysSerAlaValSerAspAsnHeAlaAspAlaIleTyrAla 367
1101 ATACCGTCCCGCTTACCATTCGCCGAAATATCCGTTCAACTTTGAGCAGC 1150
  |||||
367 sTyrProSerProTyrHisSerArgAsnIleArgSerAsnLeuIleGln 384
1151 CTTCACGCAAAAGAAACATCAGCTCTCTCAACCGTCCGCGCTCAACGCG 1200
  |||||
384 rGlyTyrGlyLysGluAsnIleThrSerSerThrValProProSerAsnGly 400
1201 AAAAATGTCAAACTGGCAGCAACGACCGACCGGAGGACGCGTACCGGT 1250
  |||||
401 LysAsnValLysLeuAlaAsnLysArgHisProLysThrLysValPro 417

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1251 TCAGCGTAAGGGTTCGAAATTTGAGAAGCAGTGAATATGATGCA 1300
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417 eAspGlyLysGlyPheProAsnPhcIuLysAspValLysTyrAspThrA 434
1301 AGCTCCAT.....ATTCAAGAATTATCGGGGGCGGTACCTAAGCT 1344
|||||
434 rGlleAsnThrAlaValProGlnValAsn.....ProIleAsp 446
1345 AACCCGTGTGTGATGCGAA.....CCGAGATGGA 1376
|||||
447 GluProValPheAsnProLysGlySerValGlySerAlaHisSerTyrPse 463
1377 GGTGTGATAGACCTTAAT.....AAATTGACACCTCGTGACAGCTGG 1420
|||||
463 rIleThrAlaArgIleGlnTyrAlaLysLeuProArgGlnGlyArgIleA 480
1421 AG.....AAAAATGTCAGGAACGAGA..... 1443
|||||
480 rGlyrIleProProLysAsnTyrSerProSerAlaProLeuProLysGly 496
1443 ..... 1443
497 ProAsnAsnGlyTyrLeuAspLysPheGlyAsnGlnTyrThrLysGlyP 513
1444 .AGAGAGAGTACAGAGTACGATTAAAGCCATGCGCA..... 1482
|||||
513 oSerArgTThrLysGlyGlnGlnPheGluTyrAspValGlnLeuSerLysT 530
1483 .....CGAGAA.....TGGGAAATTAACACAGCGTTAGCTTTAAT 1518
|||||
530 hrGlyArgGlyGlnLeuGlyTyrPalaSerArgAspGlyLysHisLeuAsn 546
1519 CATTTTACGTGTGATATCATTAAGAA 1548
|||||
547 IleSerIleAspLysIleThrHisLys 556

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seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAU27597

seq\_documentation block:

ID AAU27597 standard: Protein; 672 AA.

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XX AC AAU27597;
XX DT 18-DEC-2001 (first entry)
XX DE Neisseria meningitidis fusion protein ORF46.1-741.
XX KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX KW Neisseria protein.
XX OS Neisseria meningitidis.
XX OS Synthetic.
XX PN WO200164922-A2.
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-1B00452.
XX PR 28-FEB-2000; 2000GB-0004695.
XX PR 13-NOV-2000; 2000GB-0027675.
XX PA (CHTR-) CHIRON SPA.
XX PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MM;
XX PI Pizsa M;
XX WPI: 2001-582163/65.
XX DR N-PSDB; AAS43894.
XX PT Producing heterologous proteins from Neisseria meningitidis and N.
XX gonorrhoeae -

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PS Example 23; Page 64; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisseria proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisseria proteins. Also, a region of a protein, such as a polypeptide
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisseria proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 672 AA:

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alignment\_scores:

Quality	Length
2146.00	564
Ratio: 4.443	Gaps: 9
Percent Similarity: 85.638	Percent Identity: 77.128

alignment\_block:

US-09-303-518D-463 x AAU27597 ..

Align seg 1/1 to: AAU27597 from: 1 to: 672

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123 TTTTCGACCGCAGGGAATACACCTATTGCGCAGCAGGGGGAGCTTG 172
|||||
18 sPheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyLeuA 35
173 CCNACGCGACGCGCATATCGATTGGCAACATPACAAGCCATCAGT 222
|||||
35 laGlaArgSerIleHisIleGlyLeuGlyLysIleGlnSerHisIleLeu 51
223 GGCACCTGATGATTCACACAGCGCGCTTGAGGAATATCGGTACAT 272
|||||
52 GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTyrI 68
273 TGTCCGCTTTTCCGATCACGGGCGACAAATTCATGCCCTTGACAAC 322
|||||
68 eValAlaTrpPheSerAspHisGlyHisGlyValHisSerProPheAsn 85
323 ATGCCTACATTCGATTCGTGACGAAGCGGTAGTCCGTTGACGAGAT 372
|||||
85 IsAlaSerHisSerAspSerAspGlnIleGlySerProValAspLysPhe 101
373 AGCCCTTACCGCATCCATTGGAGGATACGAACCATCCCGCGAGCG 422
|||||
102 SerLeuTyrArgIleHisIleIleIleIleIleIleIleIleIleIle 118
423 CTATGACGGGCGACAGGGCGGCGCTATCCGCTCCAAAGCGGAGG 472
|||||
118 YTrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 135
473 ATATATACAGCTAGACATAAAGCGGTTGCCCAATATCGCTCAAC 522
|||||
135 spIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151
523 CTGACCGGACAGCGCAGCGACGACAGCGCTTGCGACCGTTCCACA 572
|||||
152 LeuThrAspAsnArgSerThrIleGlnArgLeuAlaAspArgPheHis 168
573 TCACGCGCTATGCTGACGCAAGAGTAGGCGACGATTAACCGCGCA 622
|||||
168 naIleGlySerMetLeuThrGlnGlyValGlyAspLysPheLysArgAla 185
623 CCCGATACAGCCCGACGCTGACAGATGCGGCAATCCCGCGAAGCTTC 672
|||||
185 hrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIleGlnAlaPhe 201

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[illegible]

```

1558 ACAGGAGGG...CATAGTCAACCGGTGGTATGTACAGGGAGTACCAAC 1604
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494  ASPLGylGlnLeuIleThrLeuIleSerGlyGlnPheGlnValTyrLysGI 510
      ::|||      ::|||      ::|||      ::|||      ::|||
1605 AACCTCGGCACCTGATTAACATGAGGGGTTTATCAACGC.....ACAGTGG 1648
      |||      ::|||      ::|||      ::|||      ::|||
510  Iser.....HisSerAlaLeuThrAlaPheGlnThrLug 522
      ::|||      ::|||      ::|||      ::|||      ::|||
1649 AATTTAAAAAGCCTGATGAGACTTGGAGGTGAAAAACAAAAAAGCT... 1695
      ::|||      ::|||      ::|||      ::|||      ::|||
522  InIleGlnAspSerGlnHisSerGlyLysMetValAlaLysArgGlnPhe 538
      ::|||      ::|||      ::|||      ::|||      ::|||
1696 .....GGGAAGTGTATGCACACAGCACACCATGTCCCAAAA 1731
      ::|||      ::|||      ::|||      ::|||      ::|||
539  ArgIleGlyAspIleAlaGlyGlnHisThrSerPheAspLys 552

seq_name: /SIDS1/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT:AAE10032
seq_documentation_block:
ID  AAE10032 standard; Protein: 672 AA.
xx
xx  AAE10032;
xx
xx  29-NOV-2001 (first entry)
xx
xx  N. meningitidis strain 2996 ORF46.1-741 fusion protein.
xx
xx  Heterologous expression; Neisseria protein; open reading frame; ORF;
xx  ORF46.1-741 fusion protein.
xx
xx  Neisseria meningitidis 2996.
xx
xx  WO200164920-A2.
xx
xx  07-SEP-2001.
xx
xx  28-FEB-2001; 2001WO-IB00420.
xx
xx  28-FEB-2000; 2000GB-0004695.
xx  PR 13-NOV-2000; 2000GB-0026765.
xx
xx  (CHIR-) CHIRON SPA.
xx
xx  Arico MB, Comanducci M, Galeotti C, Massignani V, Giuliani MM;
xx  P1 P1a M;
xx
xx  WPI: 2001-557776/62.
xx  DR N-FSDB; AAD17047.
xx
xx  Heterologous expression for the expression of two or more Neisseria
xx  proteins in fused state -
xx
xx  Claim 18; Page 25; 52pp; English.
xx
xx  The present invention relates to a method for simultaneous heterologous
xx  expression of two or more Neisseria proteins which are in a fused
xx  state. The method is useful for simultaneous heterologous expression of
xx  two or more Neisseria proteins. A protein that may be unstable or
xx  poorly expressed on its own is assisted by adding a suitable hybrid
xx  partner and commercial manufacture is simplified-only one expression
xx  and purification need to be employed in order to produce two separately-
xx  useful proteins. The present sequence is Neisseria meningitidis
xx  (serogroup B, strain 2996) ORF46.1 (open reading frame)-741 fusion
xx  protein.
xx
SQ  Sequence 672 AA;

alignment_scores:
      Quality: 2146.00      Length: 564
      Ratio: 4.443      Gaps: 9
Percent Similarity: 85.638      Percent Identity: 77.128

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alignment\_block:  
us-09-303-518d-463 x AAE10032 ..

Align seg 1/1 to: AAE10032 from: 1 to: 672

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2 SeraspLeuAlaAsnSperPheIleArgInValLeuAspArgInI 18
123 TTTCGAAACCGGAGGAAATACCACTATTCGGCAGCAGGGGAGACTTG 172
   |||||
18 sPheGluProAspGlyLysTyrHisLeuPheGlySerArgGlyGluLeuA 35
173 CCNAGCCGCAAGCCGATTCGATTCGGGAAACATACAAAGCCATCAGTTG 222
   |||||
35 laGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51
223 GGGCAGCTGATGATTCACAGCGCGCGCTTGAAGAAATATCGCTACAT 272
   |||||
52 GlYAsnLeuMetIleGlnGlnAlaIleIleGlyAsnIleGlyTyrI 68
273 TGTCGGCTTTCCGATCAGCGGCAAAATTCATTGCCCTTCGACACAC 322
   |||||
68 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspAsn 85
323 ATGCTTCACATTCGATTCGACGAGCGCGTTCGCCGTTGACGAGATTG 372
   |||||
85 IsAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 101
373 AGGCTTACCGCATTCATTCGGAGGATACGAAACACCATCCGCGCAGCG 422
   |||||
102 SerLeuTyrArgIleHisTyrAspGlyTyrGlnHisIleProAlaAsp 118
423 CTATGAGCGGCGCAGCGCGCGCTATCCGCTCCCAAGCGCGCAGGG 472
   |||||
118 YTYrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 135
473 ATATATACAGCTACGACATTAAGCGGCTTCGCCAAATATCCGCTCAC 522
   |||||
135 splIeTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151
523 CTGACGCAACCGCAGCAGCGGAGCAACGGCTTCGCCGCTTTCACAA 572
   |||||
152 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 168
573 TGCGGGCGCTATGCTGACGCAAGAGATGAGCGAGATTCACAGCGCCA 622
   |||||
168 naIaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 185
623 CCCGATACAGCCCGGAGCTGGACAGATCGGCAATGCGCGCAAGCCTTC 672
   |||||
185 hrArgTyrSerProGluLeuAspArgSerGlyAsnAlaIaGluAlaPhe 201
673 AACGGCAGCTCAGATATCGTCAAAAACATCATCGCGCGCGCAGAGAAAT 722
   |||||
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaIaGlyGluI 218
723 TGTCGGCGGAGCGGATCCCTGAGGGTATACGAAAGGCTCAAAATTG 772
   |||||
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIleA 235
773 CTGTCATGACAGCGCTGGGTCTGCTTTCACGAAAAACAAGATGGCGCG 822
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235 laValMetHisGlyLeuGlyLeuLeuSerThrLysAsnLysMetAlaArg 251
823 ATCAACGATTTGGCAGATATGGCGCAACTCAAAAGACTATGCCAGCAGC 872
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252 IleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaIaAla 268
873 CATCCGGGATTTGGGCACTCCAAAACCCCAATGCCGCAACAAGGATGAAG 922
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268 alIeArgAspTyrAlaValGlnAsnProAsnAlaIaGlnGlyIleGluA 285

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923 CCGTCAGCAATATCTTTATGGCAGCAGCATCCCATCAAGGGATTTGAGCT 972
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285 laValSerAsnIlePheMetAlaIaIleProIleLysGlyIleGlyAla 301
973 GTCCGGGGAAATATACGCTTTGGCGGCACTACGCGCACATCTGTCAAGCG 1022
   |||||
302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLysAr 318
1023 GTCGAGATGGGCGGATCGCATTCGGGAAAGGAAATTCGCGCTCAGCG 1072
   |||||
318 gSerIleMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 335
1073 ACAATTTTCCGATCGCGCATATACGCAAAATCCGCTCCCTTACCATTC 1122
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335 sPAsnPheAlaAspAlaIaIaTyrAlaLysTyrProSerProTyrHisSer 351
1123 CGAAATATCCGTTCAACTTGGAGCAGCGTTTACGGCAAAACATATC 1172
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352 ArgAsnIleArgSerAsnLeuGlnGlnArgTyrGlyLysGluAsnIleTh 368
1173 CTCCCAACCGTCGCGCGCGCTCAACAGCGAAATGTCAAACTGGCAGACC 1222
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368 fSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
1223 AACGCCACCGCAGACAGCGCTACCGCTTTCAGCGGTAAGGGTTCCGAT 1272
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385 InArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTGAGAACGACGTGAAATATGATACGAGCTCGATATTCAGAAATTATC 1322
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402 PheGluLysHisValLysTyrAspThrGly.....Se 412
1323 GGGGGCGGTATACCTAAGCT.....AAGCTGTGTTGATGCG. 1362
   |||||
412 rGlyGlyGlyGlyValAlaAlaAspIleGlyAlaGlyLeuAlaAspAla 429
1363 .....AAACGAGATGGAGGTTGATAGGAAGCTTAATAATTGCAACT 1407
   |||||
429 euThrAlaProLeuAspHisLysAspLysGlyLeuGlnSerLeuThrLeu 445
1408 CGTGACGAGGTGGAGAAATGTTTCAGGAACGAGACAGAGATGACAG 1457
   |||||
446 AspGlnSerValArgLysAsn...GluLysLeuLysLeuAlaIaGlnG 461
1458 TGTCGAGTTTAAAGCCCATGCGCACAGCAAGATGGGAAATTAACAGGCT 1507
   |||||
461 yAlaGlu...LysThrTyrGlyAsnGlyAspSerLeuAsnThrGlyLys 477
1508 TAGATTTTAAATCATTTTATAGGTGGTATATCAATTAAGAAAGCACAGTA 1557
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477 euLysAsnAspLysValSerArgPheAspPheIleArgGlnIleGluVal 493
1558 ACAGAGAGG...CAATGCTTAACCCGCTGATGATGACGGGTATACACA 1604
   |||||
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1605 AACCTCGGACCTCGATTAACATGAGGGTTATCAACGC.....ACAGCG 1648
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1649 AAATTAATAAAGCCTGATGAGATTTGGAGGTGGAACGAAACGAAAGAGT... 1695
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522 InIleGlnAspSerGlnHisSerGlyLysMetValAlaLysArgGlnPhe 538
1696 .....GGGAAAGTATGACACAGCAGACCATGTTCCCAAAA 1731
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539 ArgIleGlyAspIleAlaGlyGlnHisThrSerPheAspLys 552
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ID AAU27599 standard; Protein: 751 AA.
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1223 AACGCCACCCGAAGACAGCGCTACCGTTGACGGTAAGGGTTCCGAAT 1272
1224 |||||
385 InArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTGACAGCAGCGTGAATATGATACGACGTCGATATTCAGATTTATC 1322
1274 |||||
402 PheGlyLysHisValLysThrAspThrGlyLysLysLysLysLysLys 412
1323 GGGGGCGGTATATACCTAAGCTAAGCGTGTGTTGATGCGAAACCGAGAT 1372
1324 |||||
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1373 GGGAGGTGATGAGAGCTTAAATTAATGACAACTCGTGACGAGGTGAG 1422
1423 |||||
416 .....GlyAlaThrAsnAspAspValLys 424
1423 AAAAATGTTCAAGAACGAGAACGAGACGACAGTACAGTCAATTAAGC 1472
1424 |||||
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1473 CCATGCGCAACGAGAAATGGGAAATTAACAGGTTAGATTTAATCAT 1522
1474 |||||
438 .....GlyGlnGlnIleAsnGlyP 444
1523 TTTATAGTGTGCT.....GATATCAATTAAGAACGCAACGATAC 1560
1524 |||||
444 heLysAlaGlyGlnThrIleTyrAspIleAspGlnLysGlyThrIleThr 460
1561 GAGAGGCGATCTACCCGTTGGTGTATGATGATGATGATGATGATGATG 1610
1611 .....
461 ...LysLysAspAlaThrAlaAlaAspValGluAlaAspAspPheLysG 476
1611 GGCACCTGATTAACATGGGTTTATCAACGACAGTGAATTAATAAAC 1660
1612 |||||
476 yLeuGlyLysLysLysValValThrAsnLysThrLysThrValAsnGlu 493
1661 CTGATGGAAGTGGAGGTGAAACGAAACGAAACGAAAGTGAAGTGAAC 1710
1711 .....
493 snLysGlnAsnValAspAlaLysValLysAlaLysGlnLysGlnLys 509
1711 AACGACACCATGTTCCCAAAAGATGGAGCTAGAGTGAATTAAGGCTGA 1760
1712 |||||
510 LysLeuThrThrLysLeuAlaAspThrAspAlaAla.....LeuAlaAs 524
1761 AGTTACTTCGCTTGGGAAAGTAGAATAATGCTTAAGATTAATAATGCG 1810
1811 .....
524 pThrAspAlaAla.....LeuAspAlaThrThr 534
1811 AGGTTACAGTAATCGGCTATTAATAATGAGAGATTTACCGACCTAAT 1860
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1861 AGACA 1866
551 LysThr 552

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seq\_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAE10034

seq\_documentation\_block:

ID AAE10034 standard; Protein: 751 AA.

XX AAE10034;

XX 29-NOV-2001 (first entry)

XX N. meningitidis strain 2996 ORF46.1-961c fusion protein.

XX Heterologous expression: Neisserial protein; open reading frame; ORF;

XX ORF46.1-961c fusion protein.

KW

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XX OS Neisseria meningitidis 2996.
XX PN WO200164920-A2.
XX PD 07-SEP-2001.
XX PE 28-FEB-2001; 2001WO-IB00420.
XX PR 28-FEB-2000; 2000GB-0004695.
XX PR 13-NOV-2000; 2000GB-0027675.
XX PA (CHIR-) CHIRON SPA.
XX PI Arico MB, Comanducci M, Galeotti C, Mesigiani V, Giuliani MM;
XX PI Pizsa M;
XX DR WPI; 2001-557776/62.
XX DR N-PSDB; AAD17049.
XX PT Heterologous expression for the expression of two or more Neisserial
XX proteins in fused state
XX PS Claim 18; Page 26; 52pp; English.
XX CC The present invention relates to a method for simultaneous heterologous
XX expression of two or more Neisserial proteins which are in a fused
XX state. The method is useful for simultaneous heterologous expression of
XX two or more Neisserial proteins. A protein that may be unstable or
XX poorly expressed on its own is assisted by adding a suitable hybrid
XX partner and commercial manufacture is simplified-only one expression and
XX purification need to be employed in order to produce two separately-
XX useful proteins. The present sequence is Neisseria meningitidis
XX (serogroup B, strain 2996) ORF46.1 (open reading frame)-961c fusion
XX protein.
XX Sequence 751 AA;
XX SQ

```

#### alignment\_scores:

Quality: 2133.50 Length: 602  
Ratio: 4.390 Gaps: 7  
Percent Similarity: 80.731 Percent Identity: 72.425

#### alignment\_block:

US-09-303-518D-463 x AAE10034 ..

Align seg 1/1 to: AAE10034 from: 1 to: 751

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73 TCAGATTGGCAACGATCCCTTATCCGCGAGTTCGACCGTCAGCA 122
74 |||||
2 SerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgGlnI 18
123 TTTGCAACCCGACGGGAAATACACACCTATTGCGGACGAGGGAGCTTG 172
124 |||||
18 sPheGlnProAspGlyLysTyrHisLysLeuPheGlySerArgGlyLysLeu 35
173 CCNAGCGCAAGCGGCATTCGATTCGGAATTAAGCAAGCCATCAGTGG 222
174 |||||
35 IagLysArgSerLysHisLysLeuGlyLysLysLysLysLysLysLysLys 51
223 GGCACCATGATGATTCACACAGCGGCGCTGATAGGAATATCGGCTACAT 272
224 |||||
52 GlyAsnLeuMetIleGlnGlnAlaAlaAlaLysGlnLysLysLysLysLys 68
273 TGTCCGCTTTTCCGATCAGGGGACACAAATTCATTCGCTTCGACAAAC 322
274 |||||
68 eValArgPheSerAspHisGlyHisGlnValHisSerProPheAspAsn 85
323 AMGCTCACATTCCGATTCGACGAAAGCGGCTAGCCGCTGACGAGTTC 372
324 |||||
85 IAlaSerHisSerAspSerAspGlnLysSerProValAspGlyPhe 101

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373 AGCCTTTACCGCATTCATTGGAGGAGATACGAACACCATCCGCGCAGCG 422
|||||
102 SerLeuTyrTrpGlnIleHisThrAspArgIleTyrGlnHisIleProAlaAsp 118
|||||
423 CTATGACGGGCGCACAGGGGGCGGCTATCCGCTCCCAAGCGCGCAGGG 472
|||||
118 YTrpAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArg 135
|||||
473 ATATATACAGCTACGACATAAAGCGCTTGCCTCAAAATATCCGCTCAAC 522
|||||
135 spLeuTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLysAsn 151
|||||
523 CTACCGACACACCGACAGACCGGACAGCGCTTCCGACGTTTCCACAA 572
|||||
152 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHis 168
|||||
573 TGGCGGCGATGCTGACGCAAGGAGTAGCGGACGATCAACAGCGCCA 622
|||||
168 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 185
|||||
623 CCCGATACAGCCCCGAGCTGACAGATCGGCAATCGCGCAGCGCTTC 672
|||||
185 hTrpArgTyrSerProGlnLeuAspArgSerGlyAsnAlaAlaGlnAlaPhe 201
|||||
673 AACGGCAGCTGCAGATATCGTCAAAACATCATCGCGCGCGCAGGAAGAT 722
|||||
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyGln 218
|||||
723 TGTGCGCGAGGAGGATCGCGGCTATAGCGCAAGCGCTCAACATG 772
|||||
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIle 235
|||||
773 CTGTCTACGACGCGCTTGGCTCTGCTTCCACCGAAACAGATGGCGCG 822
|||||
235 lValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 251
|||||
823 ATCAACGATTTGGCAGATATGGCGCACTCAAAAGACTATCCGCGCAGC 872
|||||
252 lLeAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAla 268
|||||
873 CATCCGCGATTTGGCGAGTCCCAAAACCCCAAGCGCGCAAGCATAGAG 922
|||||
268 alIleArgAspTyrAlaValGlnAsnProAsnAlaAlaGlnGlyIleGlu 285
|||||
923 CCGTCAGCAATATCTTTATGGCAGCCATCCCATCAAAAGAGTTGGAGCT 972
|||||
285 lValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGlyAla 301
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973 GTCCGGGGGAAATAGCGCTTGGCGCGCATCAGCAGCATCTGTCAAGCG 1022
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302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLys 318
|||||
1023 GTTCGAGATGGCGGATGCGATTGGCAAGGAAATCCGCGCTCAGCG 1072
|||||
318 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSer 335
|||||
1073 ACAATTTTCCGATGGCGGATAGCGCAATATCCGCTCCCTTACCATTC 1122
|||||
335 spAsnPheAlaAspAlaAlaTyrAlaLysTyrProSerProTyrHisSer 351
|||||
1123 CGAAATATCCGTTCAAACTTGGAGCAGCGTTACGGCAAAAGAAACATCNC 1172
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352 ArgAsnIleLeuArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleThr 368
|||||
1173 CTCTCTAACCGTGGCGCGCTCAAAAGCGCAAAATGTCAAACTGAGAGAC 1222
|||||
368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
|||||
1223 AACGCCACCGAAGACAGCGCTACCGTTGACGCTAAAGGGTTCCGAT 1272
|||||
385 lArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
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1273 TTTGAGAACGACGTGAATATGATACGAAGCTCGATATTCAGAAATTATC 1322

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|||||
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412 rGlyGlyGly..... 415
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1373 GGGAGTTGATAGAGCTTAAATTAATGACACACTCGAGCAGTGAG 1422
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416 .....GlyAlaThrAsnAspAspValLys 424
|||||
1423 AAAAATGTTACGAACGAGAGAAGAGTCAGATGATGATTAAGC 1472
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425 LysAlaAlaThrValAlaIleAlaAlaAlaTyrAsnAsn..... 437
|||||
1473 CCATGCGCAGACGAGAAATGGCAAAATTAACAGCGTTGATTATTAATCAT 1522
|||||
438 .....GlyGlnGlnLysAsnGly 444
|||||
1523 TTATAGTGCT.....GATATCAATAAGAAAGCACAGTAA 1560
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444 hEysAlaGlyGlnThrIleTyrAspIleAspGlnAspGlyThrIleThr 460
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1561 GGAGGCACTACTTAACCCGTGTGATGATAGGGGTGATACACAAACCTTC 1610
|||||
461 ..LysLysAspAlaThrAlaAlaAspValGlnAlaAspAspPheLysGly 476
|||||
1611 GGCACCTGATACATAGGCGTTTATCAAGCAGCAGCTGCAATTAATAAGC 1660
|||||
476 YLeuGlyLeuLysLysValValThrAsnLeuThrLysThrValAsnGlu 493
|||||
1661 CTGATGAGAGTTGGAGGTGAAAGCAAAAGGTGGAAAGTGATGACC 1710
|||||
493 snLysGlnAsnValAspAlaLysValLysAlaAlaGlnSerGlnIleGlu 509
|||||
1711 AAGCACACCATGTTCCCAAAAGATTTGGATGAGGCTGAATTAGCGCTCA 1760
|||||
510 LysLeuThrThrLysLeuAlaAspThrAspAlaAla.....LeuAlaAs 524
|||||
1761 AGTACTCTGGCGCTGGCAAGTACAAATATGCTTAACGATATAATAATGCG 1810
|||||
524 PThrAspAlaAla.....LeuAspAlaThrThr 534
|||||
1811 AGGTTACAGTAATAATCGGATTAATAATAAGAGATTATACCGAATTAAT 1860
|||||
534 snAlaLeuAsnLysLeuGlyGlnAsnIleThrThrPheAlaGlnGlnThr 550
|||||
1861 AGANCA 1866
|||||
551 LysThr 552
|||||
seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU27598
seq_documentation_block:
ID AAU27598 standard; Protein; 806 AA.
XX
AC AAU27598;
XX
DT 18-DEC-2001 (first entry)
XX
DE Neisseria meningitidis fusion protein ORF46.1-961.
XX
KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
KW Neisserial protein.
XX
OS Neisseria meningitidis.
XX
Synthetic.
XX
PN WO200164922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00452.

```



XX 28-FEB-2000; 2000GB-0004695.  
PR 13-NOV-2000; 2000GB-0027675.  
XX  
XX (CHIR-) CHIRON SPA.  
XX Arico MB, Comanducci M, Galeotti C, Massignani V, Guillian MM;  
PI Pizze M;  
XX  
XX MPI: 2001-582163/65.  
DR N-PSDB; AAS43895.  
XX  
XX Producing heterologous proteins from *Neisseria meningitidis* and *N.*  
PT gonorrhoeae -  
XX  
XX Example 23; Page 65; 119pp; English.  
PS  
XX The invention relates to methods for the heterologous expression of  
CC Neisserial proteins from *Neisseria meningitidis* and *Neisseria*  
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the  
CC leader peptide, and may be replaced by a domain from a different protein  
CC to make a fusion protein. In order to enhance heterologous expression of  
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine  
CC stretch, can be mutated to enhance expression. The proteins used in the  
CC processes include ORF4.1, 287, 741, 919, 953, 961 and 983. Sequences  
CC AAU27553-AAU27610 represent *Neisseria* proteins and peptide regions of  
CC proteins of the invention.  
XX  
XX Sequence 806 AA:

alignment\_scores:  
Quality: 2133.50 Length: 602  
Ratio: 4.390 Gaps: 7  
Percent Similarity: 80.731 Percent Identity: 72.425

alignment\_block:

US-09-303-518D-463 x AAU27598 ..

Align seg 1/1 to: AAU27598 from: 1 to: 806

73 TCAGATTGGCAACGATCCCTTATCGCGAGGTTCGACCGTCAGCA 122  
|||||  
2 SerAspLeuAlaAsnSerPheIleArgIleValLeuAspArgIle 18  
123 TTTCGACCCGACGGGAAATACCACTATTCGGCAGCGGGAGCTTG 172  
|||||  
18 SPhgIuProAspIleLysIleArgIleValLeuAspArgIle 35  
173 CCNAGCCGACGCGCATATCGATTGGGAAACATACAAAGCCATCAGTTG 222  
|||||  
35 IagIuArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51  
223 GGCACCTGATGATTAACAGCGCGCTTGAAGAAATATCGGCTACAT 272  
|||||  
52 G1YAsnLeuMetIleGlnIleAlaIleLeuGlyAsnIleGlyTyrI 68  
273 TGTCCGCTTTCGATCAGCGGACAAATCCATTCGCGCTTGACAAAC 322  
|||||  
68 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspS 85  
323 ATGCTACATTCGATTCGACAGCGCGGTAGTCCGTTGACGAGATTC 372  
|||||  
85 IAlaSerHisSerAspSerAspIleValIleGlySerProValAspGlyPhe 101  
373 AGCTTACCGCATTCATTTGGAGCGATACGAACACCATCCGCGCAGG 422  
|||||  
102 SerLeuTyrArgIleHisIleTyrAspGlyTyrGlnHisIleProAlaAspGly 118  
423 CTATGAGGGCGCAGGGCGCGCTATCCCGCCCAAGGGCGGAGG 472  
|||||  
118 YTYAspIleProGlnIleGlyLysIleTyrProAlaProLysGlyAlaArg 135

473 ATATATACAGCTACGACATAAAGCGTTGCCCAAAATATCCGCTCAAC 522  
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135 SPLeTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151  
523 CTGACCGACAAACCGGACGCGGACAAAGCGTTCCGACCTTCCCA 572  
|||||  
152 LeuTyrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHis 168  
573 TGCCGCGCTATGCTGACGCAAGGAGTAGGCGGAGGATTCAAAGCGCA 622  
|||||  
168 nAlaIleSerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 185  
623 CCGATACAGCCCGGACGCTGACAGATCGGCAATCCCGCGAAGCTTC 672  
|||||  
185 hrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIleAlaPhe 201  
673 AACGCACTGCGATATGCTCAAAAACATCATCGCGCGGCGGAGGAAAT 722  
|||||  
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyIle 218  
723 TGTCCGCGGAGCGATGCGCGTGCAGGATATGAGCGAAGCTCAAAAT 772  
|||||  
218 eValIleGlyAlaGlyAspAlaValGlnGlyIleSerGlnLysSerHis 235  
773 CTGTATGACAGCGCTGGGCTGCTTTCACCGAAACAGATGGCGCGC 822  
|||||  
235 IAlaMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 251  
823 ATCAACGATTTGGCAGATATGCGGCACTCAAGCTATGCGGACGACG 872  
|||||  
252 ILeAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAla 268  
873 CATCCGCGATTGGCAGTCGCAAAACCCCAATCCGCGCAAGGATAGAG 922  
|||||  
268 AlLehrArgAspTrpAlaValGlnAsnProAsnAlaIleGlnGlyLeu 285  
923 CCGTACGACATATCTTTATGCGACCATCCCATCAAGGATTTGAGCT 972  
|||||  
285 IAlaValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGly 301  
973 GTCCGGGGAAATACGGCTTGGCGGCGCATACGCGCATCTGTCAGACG 1022  
|||||  
302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLys 318  
1023 GTCCGAGATGGCGCGCATGCGCATTCGCCAAAGGAAATCCGCGTCA 1072  
|||||  
318 GSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerHisValSer 335  
1073 ACAATTTTGGCGATGCGGATACGCCCAATVACCGCTCCCTTACCAT 1122  
|||||  
1123 CGAATATTCGTTCAAACTTGGACGACGCTTACGGCAAAAGAAATAC 1172  
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352 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleThr 368  
1173 CTCCTCAACCGTGGCGCGCTCAAAAGCGCAAAATATCAAACTGGAGAC 1222  
|||||  
368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAsp 385  
1223 AACGCCACCGCAAGACAGCGTACCGTTGACGCTAAAGGCTTCCGAT 1272  
|||||  
385 IArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401  
1273 TTTCGACACACGTAATATGATACGAAGCTCGATATTCAGAGATTTTC 1322  
|||||  
402 PheGlnLysHisValLysTyrAspThrGly.....Se 412  
1323 GGGGGCGCGGTATACCTAAGGCTATGCTGTGTTGATGGCAACCGAGAT 1372  
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412 rGlyGlyGly..... 415  
1373 GGGAGGTTGATAGAAAGCTTAATAATTGACAACCTGTCGACGAGGTGAG 1422



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|||||.....|
168 nalaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAlaT 185
623 CCGGATACAGCCCGAGCTGAGCAGATCGGAGCAATGCGCGCGAAGCTTC 672
185 htrGlyTyrSerProGluLeuAspArgSerGlyAsnAlaAlaGluAlaPhe 201
673 AACGGCAGCTGCAGATATGTCAAAAACATCATGCGCGCGAGCAGAGAAAT 722
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaIleGlyLul 218
723 TGTGCGGCGAGCGGATGCCGTGAGGGTATACGGAAGCTCAACATTG 772
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGluGlySerAsnIleA 235
773 CTGTCAATGCAGCGCTGGCTGTCTTCCACCGAAAAACAAGATGGCGCG 822
235 lValIleMetHisGlyLeuGlyLeuLeuSerThrGluAsnLysMetAlaArg 251
823 ATCAACGATTGGCAGATATGCGCAACTCAAGACTATGCCGACAGCAG 872
252 IleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaIleAla 268
873 CATCCGCGATTGGGCGAGTCCAAAACCCCAATGCCGACAGGATGAAG 922
268 aIleAlaGAspTyrAlaValGlnAsnProAsnAlaIleGlnGlyIleGluA 285
923 CCGTCAGCAATATCTTATGCGAGCCATCCCATCAAGGATGGAGGT 972
285 lValIleSerAsnIlePheMetAlaIleIleProIleLysGlyIleGlyAla 301
973 GTCCGGGGAAATATCGGCTTGGGCGCATCAGCGCAGATCTGTCAAGCG 1022
302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLysArg 318
1023 GTGCGAGATGGCGCGATCGCATGCGGAAAGGAAATCCCGCTGACGG 1072
318 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValIleSerA 335
1073 ACAATTTGGCGATGCGGATACGCCAAATACCCCTCCCTTAACCTTCC 1122
335 sPasnPheAlaAspAlaIleTyrAlaIleLysTyrProSerProTyrHisSer 351
1123 CGAAATATCCGTTCAACTTGGAGCAGCGTTACGCCAAAGAAACATCAC 1172
352 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGluAsnIleTh 368
1173 CTGCTCAACCGTGGCGCGTCAACGCGCAAAAATGTCAACTGGCAGACC 1222
368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
1223 AACGCCACCGAAGACAGCGGTACGCTTGAAGGTAAAGGTTTCGAGT 1272
385 lnaArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTGAGAACGACGTGAATATGATACGAAGCTCGATATTTCAAGAAATATC 1322
402 PheGluLysHisValLysTyrAspThrGly.....Se 412
1323 GGGGGCGGTATACCTAAGGCTAAGCGTGTGTTGATCGGAACCGAGAT 1372
412 rGlyGlyGly..... 415
1373 GGGAGCTGTATAGAGCTTAATTAATTGACAACCTGTGAGCAGGTGAG 1422
416 .....GlyAlaThrAsnAspAspValLys 424
1423 AAAAATGTTCAAGAAACGAAAGAGAGCTCAGAGTAGTCACTTTAAAC 1472
425 LysAlaIleThrValAlaIleAlaIleAlaIleTyrAsnAsn..... 437
1473 CCATGGGCAACGAGATGGAAATTAACAGGTTAGTTTAAATCAT 1522
|||||.....|

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438 .....GlyGlnGluIleAsnGly 444
1523 TTATAGTGT.....GATATCATTAAGAAAGCAGCTACA 1560
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444 heLysAlaGlyGluThrIleTyrAspIleAspGluAspGlyThrIleThr 460
1561 GGAGGCGATAGTCTAACCCGTGTGATGTACGGGTGATACAAACCTC 1610
461 ...LysLysAspAlaThrAlaAlaAspValGluAlaAspAspPheLysG 476
1611 GCCACCTGATTAACATGGGCTTTATCAAGCAGACGTGGAATTAAGAAC 1660
476 YLeuGlyLeuLysLysValIleThrAsnLeuThrLysThrValAsnGluA 493
1661 CTGATGGAAGTGGAGGTGAAGAAAGGGAAGGGAAGTATGACC 1710
493 snLysGlnAsnValAspAlaLysValLysAlaAlaGluSerGluIleGlu 509
1711 AAGCACACCATGTTCCCAAAAGATTGGATGAGGCTGATTAAGGCTGA 1760
510 LysLeuThrThrLysLeuAlaAspThrAspAlaIle.....LeuAlaAs 524
1761 AGTTACTTCGCTTGGCAAGTACATATATGCTTAAGGATTAATTAAGGC 1810
524 PThrAspAlaIle.....LeuAspAlaThrThrA 534
1811 AGGGTACAAGTAAATCGGGTATTAATAGAAGATTACCGAACCTAAT 1860
534 snAlaLeuAsnLysLeuGlyGluAsnIleThrThrPheAlaGluGluThr 550
1861 AGACA 1866
551 LysThr 552

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seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA27582

seq\_documentation\_block:

ID AAU27582 standard; Protein; 675 AA.

AC AAU27582;

DT 18-DEC-2001 (first entry)

DE Neisseria meningitidis fusion protein delta-G741-ORP46.1.

KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORP46.1;

KW Neisseria meningitidis.

OS Neisseria meningitidis.

PN NO200164922-A2.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001MO-IB00452.

PR 28-FEB-2000; 2000GB-0004695.

PR 13-NOV-2000; 2000GB-0027675.

PA (CHIR-) CHIRON SPA.

PI Arico MB, Comanducci M, Galeotti C, Mesigiani V, Gulliani MM;

PI Pizza M;

DR WPI; 2001-582163/65.

DR N-PSDB; AAS43881.

PT Producing heterologous proteins from Neisseria meningitidis and N.

PT gonorrhoeae -

PS Example 15; Page 53; 119pp; English.

XX

CC The invention relates to methods for the heterologous expression of  
 CC Neisserial proteins from Neisseria meningitidis and Neisseria  
 CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the  
 CC leader peptide, and may be replaced by a domain from a different protein  
 CC to make a fusion protein, in order to enhance heterologous expression of  
 CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine  
 CC stretch, can be mutated to enhance expression. The proteins used in the  
 CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences  
 CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of  
 CC proteins of the invention.

XX Sequence 675 AA;

# alignment\_scores:

Quality: 2112.00 Length: 410  
 Ratio: 5.189 Gaps: 0  
 Percent Similarity: 99.268 Percent Identity: 97.073

# alignment\_block:

US-09-303-518D-463 x AAU27582 ..

Align seg 1/1 to: AAU27582 from: 1 to: 675

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258 SerSeraspneuAlaasnAspserPheIleArgGlnValLeuAspArgG1 274
120 GCATTGGAAACCGGAGCGGAAATACACCTTATTCGCGAGGCGGAGC 169
   |||||||
274 nHsPheGluProaspGlyLysTyrHisLeuPheGlySerArgGlyLul 291
170 TTGCCNAGCCCAAGCGCATATCGATTGGGAAACATACAAACCATCAG 219
   |||||
291 euAlaGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 307
220 TTGGGCACTGATGATCAACAGCGCGCGTTGAAGGAATATCGGCTA 269
   |||||
308 LeuGlyAsnLeuMetIleGlnGlnAlaIleValIleGlyAsnIleGly 324
270 CATGTGCGGCTTTCGATCAGCGGCGCAAAATTCGATTCGCGCTGACA 319
   |||||||
324 rIleValArgPheSerAspHisGlyHisGluValHisSerProPheAsp 341
320 ACCATGCGCTACATTCGATTCGACGAGACCGGTAGTCCCGTTGACGGA 369
   |||||||
341 snHisAlaSerHisSerAspSerAspGlyLysIleGlySerProValAsp 357
370 TTACGCTTTACCGCATTCATTCGAGCGGATACGACACCATCCCGCGA 419
   |||||||
358 PheSerLeuTyrArgIleHisIleHisIleHisIleHisIleHisIle 374
420 CGGCTATGAGCGGCGCAGCGGCGGCTATCCCGCTCCCAAGGCGCGA 469
   |||||||
374 pGlyTyrAspGlyProGlnGlyGlyGlyTyrProAlaProLysGlyAla 391
470 GGGATATATACGCTACGACATAAAGCGCTGCGCAAAATATCCGCTC 519
   |||||||
391 rGAspIleTyrSerTyrAspIleGlyGlyAlaAlaGlnAsnIleArgLeu 407
520 AACCTGACCGAACAACCGACGCGCAACGCGCTTCCGACCGTTTCCA 569
   |||||||
408 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheH 424
570 CAATGCGGCGGCTATGCTGACGCGAAGAGTAGGAGCGATTCGAACGCG 619
   |||||||
424 sAsnAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArg 441
620 CCACCGCATACAGCCCGAGCTGAGCAGATCGGCAATCGCGCGAAGCC 669
   |||||||
441 lathrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIleGlyAla 457
670 TTCACGCGCATCGAGATATCGTCAAAAACATCATCGCGCGCGACGAGA 719

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458 PheAsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyG1 474
720 AATGTGCGCGGAGCGCATGCCGTGACGAGGTATTAAGCAAGGCTCAACA 769
474 uIleValIleGlyArgGlyAspAlaValGlnGlyIleSerIleLysSerAsn 491
770 TTGCGTATGACGACGCGCTGGCTGCTGCTTTCACCGAACAACATGAGCG 819
491 lAlaValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAla 507
820 CGCATCAACGATTTGGCAGATATGGCGCACTCAAAAGCTATGCCGACG 869
508 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAl 524
870 AGCCATCCGCGGATTTGGCAGTCCAAACCCCAATGCCGCGCACAGCATAG 919
524 aAlaIleArgAspIrrAlaValGlnAsnProAsnAlaAlaGlnGlyIleG 541
920 AAGCGTCAGCAATATCTTATGCGAGCCATCCCATCAAGAGGATTTGGA 969
541 lAlaValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGly 557
970 GCTGTCGGGGAAATACGCGCTTGGCGGCGCATCACGCGACATCTGTCAA 1019
558 AlaValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleL 574
1020 GCGGCGCAGATGGGCGGATGCGCATGCCGAAAGGAAATCCGCGCTCA 1069
574 sArgSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValS 591
1070 GCGACAAATTTTCCGATGCGGCGCATGCGCAAAATACCGCTCCCTTACAT 1119
591 eRAspAsnPheAlaAspAlaIleTyrAlaLysTyrProSerProGlyHis 607
1120 TCCCGAAATATCCGTTCAACTTGGAGCAGCGTTACGGCAAGAAACAT 1169
608 SerArgAsnIleArgSerAsnLeuGlnGlnArgTyrGlyLysGluAsnI 624
1170 CACCTCCCTCAACCGTGGCGCGCTCAACAGCGCAAAATGTCAAACTGCGAG 1219
624 eThrSerSerThrValProProSerAsnGlyLysAsnValLysLeuAla 641
1220 ACCAAGCGCACCGCAAGACAGCGGTACCGTTGACGATTAAGGCTTCCG 1269
641 sPglArgHisProLysThrGlyValProPheAspGlyLysGlyPhePro 657
1270 AATTTGAGCAAGCAGGTGAATATGATACG 1299
658 AsnPheGluLysHisValLysTyrAspThr 667

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seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAE10031

seq\_documentation\_block:

ID AAE10031 standard; Protein: 675 AA.

XX AAE10031;

AC AAE10031;

DE 29-NOV-2001 (first entry)

XX

DE N. meningitidis strain 2996 delta G741-ORF46.1 fusion protein.

KW Heterologous expression; Neisserial protein; open reading frame; ORF;

KW delta G741-ORF46.1 fusion protein.

XX

OS Neisseria meningitidis 2996.

XX

PN W0200164920-A2.

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-IB00420.

XX



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XX 18-DEC-2001 (first entry)
DT Neisseria meningitidis fusion protein delta-G983-ORF46.1.
XX
DE Neisseria gonorrhoeae: leader peptide: fusion protein; ORF46.1;
KW Neisserial protein.
XX
OS Neisseria meningitidis.
OS Synthetic.
XX
PN WO200164922-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-1B00452.
XX
PR 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MM;
PI Pizsa M;
DR MPI; 2001-582163/65.
DR N-PSDB; AAS43874.
XX
PT Producing heterologous proteins from Neisseria meningitidis and N.
PT gonorrhoeae -
XX
PS Example 15; Page 44; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisserial proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 1474 AA;
alignment_scores:
Quality: 2112.00 Length: 410
Ratio: 5.189 Gaps: 0
Percent Similarity: 99.268 Percent Identity: 97.073
alignment_block:
US-09-303-518D-463 x AAU27575 ..
Align seg 1/1 to: AAU27575 from: 1 to: 1474
70 GCCCTGACATTTGGCAAGCATCCCTTATCCGGCAGGTTCTGCACGCTCA 119
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1057 SerSerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgGln 1073
120 GCATTTCGACCCGACGGGAAATACACACTATTTCGACGAGGAGGAGG 169
|||||
1073 nHisPheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyLul 1090
170 TTGGCCNAGCCCAACGGCCATATCGATTGGGAAACATACAAAGCCATCAG 219
|||||
1090 euAlaGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 1106
220 TTGGCCACCTGATGATTCACACAGCGCGCTGCAAGGAATATCGGCTA 269
|||||
1107 LeuGlyAsnLeuMetIleGlnGlnAlaIleLeuGlyAsnIleGlyTyr 1123
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270 CATGTCCGCTTTCCGATCAGCGGACCAAAATTCATTGCGCCTTCGACA 319
|||||
1123 rIleValArgPheSerAspHisGlyHisGlnValHisSerProPheAspA 1140
320 ACCATGCTTCACATTCGATTCTGACGAAAGCCGGATGCCGTTGACGGA 369
|||||
1140 snHisAlaSerHisSerAspSerAspGlnAlaGlySerProValAspGly 1156
370 TTCAGCCTTTACCGCATCCATTCGAGGATACGAAACCAATCCCGCGCA 419
|||||
1157 PheSerLeuTyrArgIleHisIleTyrAspGlyTyrGlnHisIleProAla 1173
420 CGGCTATGACGGGCGCACAGGGCGGCGCTATCCGCTCCCAAGGCGGCA 469
|||||
1173 pGlyTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaA 1190
470 GGGATATATACAGCTACGACATAAAGCGTTCGCCAAATATCCGCTC 519
|||||
1190 rAspIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeu 1206
520 AACCTGACCGACACCGGACGACGAGACAGGCTTCGCGGACCGTTTCCA 569
|||||
1207 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheH 1223
570 CAATGCGGCGCTATGCTGACGCAAGAGTAGCGCAGGATTCAAACGCG 619
|||||
1223 sAsnAlaGlySerMetLeuThrGlnGlyValGlyLyspGlyPheLysArgA 1240
620 CCACCCGATACAGCCCCGAGCTGGACAGATCGGGCAATGCGCGCAGACC 669
|||||
1240 lAtThrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIleGlnAla 1256
670 TTCACGCGCATCTGCAGATATGCTCAAAAACATCATCGCGCGGCGAGGA 719
|||||
1257 PheAsnGlyThrAlaAspIleValAlaLysAsnIleIleGlyAlaIleGly 1273
720 AATGTGCGCGCAGCGGATGCGGTCCAGGATTAAGCAGAGGCTTCAAACA 769
|||||
1273 ulleValGlyAlaGlyAspAlaValaGlnGlyLysSerGlnGlySerAsnI 1290
770 TTGCTGTCTATGCAAGGCTTGGCTTCTGCTTTCACCGAAACAAAGTGGCG 819
|||||
1290 lAlaValaMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAla 1306
820 CGCATCAACGATTTGGCAGATATGCGCAACTCAAAAGCTATGCGCGAGC 869
|||||
1307 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAl 1323
870 AGCCATCCGCGATTGGCAGTCCAAACCCCAATGCCGACAGGCAATAG 919
|||||
1323 alAlaIleArgAspTyrPheAlaValaGlnAsnProAsnAlaIleGlnGly 1340
920 AAGCGCTCAGCAATATCTTTATGCGACGCTATCCCATCAAGGATTTGA 969
|||||
1340 lAlaValaSerAsnIlePheMetAlaAlaIleProIleLysGlyLysGly 1356
970 GCTGTCGGGGGAAATACGGGCTTGGGGGCGCATACGACATCCGTGCAA 1019
|||||
1357 AlaValaArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleL 1373
1020 GCGGTCGCGAGTGGCGGATCGCAATTGCCGAAAGGAAATCCGCGCTCA 1069
|||||
1373 sArgSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValS 1390
1070 GCGACAATTTTCCGATCGCGGACATCGCAAAATACCGCTCCCTTACAT 1119
|||||
1390 eArgAspAsnPheAlaAspAlaIleAlaTyrAlaLysTyrProSerProTyrHis 1406
1120 TCCGGAATATCCGTTCAAACTTGAGAGCAGGTTAAGGCAAAAGAAATAT 1169
|||||
1407 SerArgAsnIleLeuArgSerAsnLeuGlnGlnArgTyrGlyLysGlnAsnI 1423
1170 CACCTCTCTCAACCGTGC CGCGCTCAAAAGCGCAAAATGTCAACTGCGAG 1219
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1423 erthserThrvAlProProSeransgLyLysAsnValLysLeuAlaA 1440  
 1220 ACCAAGCCCGGAGACAGCGGTACCGTTACCGTAAAGGTTCCG 1269  
 1440 spGlnAghisProLysThgLyValProPheaspGlysgLyPhePro 1456  
 1270 AATTTTGAAGACGCTGAATATGATACG 1299  
 1457 AsnPhgLyLysHisValLysTyrAspThr 1466

seq\_name: /SIDst/gcgcdata/geneseq/geneseq\_emb1/AA2001.DAT:AAE10022

seq\_documentation\_block:

ID AAE10022 standard; Protein: 1474 AA.

AC AAE10022;

DT 29-NOV-2001 (first entry)

DE N. meningitidis strain 2996 delta G983-ORF46.1 fusion protein.

KW Heterologous expression: Neisserial protein: open reading frame: ORF:  
 delta G983-ORF46.1 fusion protein.

OS Neisseria meningitidis 2996.

PN MO200164920-A2.

PD 07-SEP-2001.

PE 28-FEB-2001; 2001WO-IB00420.

PR 28-FEB-2000; 2000GB-0004695.

PR 13-NOV-2000; 2000GB-0027675.

XX (CHIR-) CHIRON SPA.

XX Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;  
 P1 Pizze M;

XX WPI: 2001-557776/62.

DR N-PSDB; AADI7039.

XX Heterologous expression for the expression of two or more Neisserial  
 PT proteins in fused state

PS Claim 18; Page 14-15; 52pp; English.

XX The present invention relates to a method for simultaneous heterologous  
 CC expression of two or more Neisserial proteins which are in a fused  
 CC state. The method is useful for simultaneous heterologous expression of  
 CC two or more Neisserial proteins. A protein that may be unstable or  
 CC poorly expressed on its own is assisted by adding a suitable hybrid  
 CC partner and commercial manufacture is simplified-only one expression and  
 CC purification need to be employed in order to produce two separately-  
 CC useful proteins. The present sequence is Neisseria meningitidis  
 CC (serogroup B, strain 2996) delta G983-ORF46.1 (open reading frame)  
 CC fusion protein.

SO Sequence 1474 AA;

alignment\_scores:

Quality: 2112.00 Length: 410  
 Ratio: 5.189 Gaps: 0  
 Percent Similarity: 99.268 Percent Identity: 97.073

alignment\_block:

US-09-303-518D-463 x AAE10022

Align seg 1/1 to: AAE10022 from: 1 to: 1474

70 GCCTCAGATTGGCAAAACGATCCCTTATCCGCGAGGTTCTCGACGCTCA 119  
 1057 SerSerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgL 1073  
 120 GCATTTCCAGCCCGACGCGGAATACACCTATTTGGCAGCAGCGGGAGC 169  
 1073 nhIsPhgLyLysProAspGlyLysTyrHisLeuPhgLySerArgLyL 1090  
 170 TTGCGNAGCGCAGCGCATTCGATTGGGAACATACCAAGCCATCAG 219  
 1090 euAlaGlnArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 1106  
 220 TTGGCCGACCTGATGATTCACAGCGCGGTGATACAGAAATATCGGCTA 269  
 1107 LeuGlyAsnLeuMetIleGlnGlnAlaAlaIleLysGlyAsnIleGly 1123  
 270 CATTCGCGCTTTTCGATCACGGGCGCAAAATTCATTCGCGCTTCGACA 319  
 1123 rIleValArgPheSerAspHisGlyHisGlnValHisSerProPheAsp 1140  
 320 ACCATGCTCATTTCGATTCGATTCGACAGCGCGGTAGTCCGTTGACGA 369  
 1140 snHisAlaSerHisSerAspSerAspGlnAlaGlySerProValAspGly 1156  
 370 TTCAGCCCTTACCGCATTCGATTCGATTCGATTCGATTCGATTCGATTC 419  
 1157 PheSerLeuTyrArgIleHisIleTyrAspGlyTyrGlnHisSerProAlaAs 1173  
 420 CGGCTATGACGGGCGCACGGGCGGCTATCCGCTCCCAAGCGCGCA 469  
 1173 pGlyTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAla 1190  
 470 GGGATATATACAGCTACGACATTAAGCGCTGGCCCAATATCCGCTC 519  
 1190 rGAspIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeu 1206  
 520 AACCTGACCGCAACCGCAGCAGCGACAGCGCTCCGCGCGCTTCGA 569  
 1207 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheH 1223  
 570 CAATGCGGCGCTATGCTGACGCAAGATAGCGGATTCACACCG 619  
 1223 sAsnAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArg 1240  
 620 CCACCGCATACAGCCCGCAGCTGACAGATGCGGCATGCGCGGAGCC 669  
 1240 IeThrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaAlaGlyAla 1256  
 670 TTCACGGGCGCTGATGATGTCAAAACATCATTCGCGCGCGGAGAGA 719  
 1257 PheAsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGly 1273  
 720 AATTTGCGGCGCAGCGCATGCGGTGACAGGTATAGCAAGGCTCAACA 769  
 1273 uIleValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsn 1290  
 770 TTGCTGTCATGACAGCGCTGGGTGCTGCTTCACAGCAAAACAGATGCG 819  
 1290 IeAlaValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAla 1306  
 820 CGCATCAACGATTTGGCAGATATGCGCAACTCAAGCATATGCGCGAGC 869  
 1307 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAla 1323  
 870 AGCCATCCGCGATTTGGCAGTTCGCAAAACCCCAATGCGCGACAGCATAG 919  
 1323 AlaIleArgAspThrAlaValGlnAsnProAsnAlaAlaGlnGlyIleG 1340  
 920 AAGCGTCAGCATATCTTATGCGACGCAATCCCATCAAGGATTCGA 969  
 1340 IuAlaValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGly 1356  
 970 GCTGTCCGGGGAATAAGCGCTTGGCGGATCATCAGGCGACATCTGTCA 1019



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|||||
1357 Alavalarglystyrglyleuglyglylethralahisprolely 1373
1020 GCGGTGCAATATGGCCGCGCATTCGCGGAAGGGAATCGCGCTCA 1069
1373 sargsergimerclyalallealeuprolysglyyseralavalas 1390
1070 GCGCAATTTGGCGATGGCGCATACGCCAATATCCGCCCTTACCAT 1119
1390 eraspasnphelialaspalialatryalalystryproserprotyrhis 1406
1120 TCCCGAAATATCCGTTCAAACTTGAGACAGCGTTACGCCAAGAAACAT 1169
1407 SerArgasnleatrgserAsenleuglInArgtyrGlyysgluasnll 1423
1170 CACCTCTCAACGCGCGCGCTCAAAAGGCAAAATGTCAACTGGCAG 1219
1423 ethrSerSerThryalProProSerasnnglylysasnvallysluAlaA 1440
1220 ACCAGACCCAGCCGAGACAGAGCGTTCGTTGACGGTAAAGGTTCCG 1269
1440 spclnatghisprolysthnglylyalProPheaspolylysglypnepro 1456
1270 AATTTTGAGAGACAGTGAATATGATACG 1299
1457 AsnPheglulushlyshlyvallystryAspThr 1466

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seq\_name: /STDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAU27603

seq\_documentation\_block:

ID AAU27603 standard; Protein; 751 AA.

AC AAU27603;

DT 18-DEC-2001 (first entry)

DE Neisseria meningitidis fusion protein 961c-ORF46.1.

KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;

KW Neisserial protein.

OS Neisseria meningitidis.

OS Synthetic.

PN WO200164922-A2.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-IB00452.

PR 28-FEB-2000; 2000GB-0004695.

PR 13-NOV-2000; 2000GB-00287575.

PA (CHIR-) CHIRON SPA.

PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MM;

PI Pizze M;

DR MPI: 2001-582163/65.

DR N-PSDB; AAS43900.

PT Producing heterologous proteins from Neisseria meningitidis and N.

PT gonorrhoeae -

PS Example 23; Page 70-71; 119pp; English.

CC The invention relates to methods for the heterologous expression of  
 CC Neisserial proteins from Neisseria meningitidis and Neisseria  
 CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the  
 CC leader peptide, and may be replaced by a domain from a different protein  
 CC to make a fusion protein, in order to enhance heterologous expression of  
 CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine  
 CC stretch, can be mutated to enhance expression. The proteins used in the

CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences  
 CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of  
 CC proteins of the invention.

XX Sequence 751 AA:

alignment\_scores:                      Length: 409  
     Quality: 2111.00  
     Ratio: 5.200  
     Gaps: 0  
     Percent Similarity: 99.267      Percent Identity: 97.311

alignment\_block:

US-09-303-518D-463 x AAU27603

Align seg 1/1 to: AAU27603 from: 1 to: 751

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|||||
335 SerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgGlnH 351
123 TTTGCAACCCGAGGGAATACCACTTATTCGCGAGCGGGGAGGCTTG 172
|||||
351 sPheGlnProAspGlyLysTyRHisLeuPheGlySerArgGlyGluLeuA 368
|||||
173 CCNAGCGCAACGGCCATATCGGATTGGGAACATCAAAAGCCATCAGTTG 222
|||
368 IAGLIARgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 384
223 GGCACCTGATGATTCAAACAGCGCGCGCTTGACGAAATATCGCTACAT 272
|||||
385 GlyAsnLeuMetIleGlnGlnAlaIleIleLysGlysnIleGlyTyRll 401
273 TGTCCGCTTTCCGATTCACGGGCAAAATTCATTCGCGCTTGACAAAC 322
|||||
401 eValArGPheSerAspHisGlyHisGluValHisSerProPheaspasnH 418
323 ATGCTCACATTCGATTCGACGAGCGGCTAGTCCGTTGACGAGATTC 372
418 IAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 434
373 AGCCTTACCGCATTCATTGGAGCGGATAGCAACACATCCCGCGACGCG 422
435 SerLeuTyRArgGlnHisIleIleIleIleIleIleIleIleIleIleI 451
423 CTATGACGGGCGACAGCGCGGCTATCCGCTCCCAAGCGCGAGAGG 472
451 YTyRAspGlyProGlnGlyGlyTyRProAlaProLysGlyAlaArgA 468
473 ATATATACAGCTACGACATAAAGCGCTTGCCCAAAATATCCGCTCAAC 522
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468 sPleIleTySerTyRAspIleLysGlyValAlaGlnAsnIleArgLeuasn 484
523 CTGACCGACACCGCGACAGCGGACACGCGCTTGCGGACCGTTCCCAAA 572
485 LeuThrAspAsnArgSerThrclyGlnArgLeuAlaAspArgPheHisAs 501
573 TGC CGCGCTATGCTGACGCAAGAGTAGCGGACGAGTTCAAAGCGCGCA 622
501 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAlat 518
623 CCCGATACAGCCCGAGCTGACAGATCGGGCAATGCCCGGAAGCTTCG 672
518 hrArgTyRserProGluLeuAspArgSerGlyAsnAlaAlaGlnAlaPhe 534
673 AACGCGACTGCAGATATGTCAAAACATCATCGCGCGGCGAGAGAAAT 722
535 AsnGlyThrAlaAspIleValLysasnIleIleGlyAlaAlaGlyGluI 551
723 TGTCCGCGAGCGAGTCCGTCAGAGTATAGCAAGCAAGCTCAAAACATG 772
551 eValGlyAlaGlyAspAlaValAlaGlnGlyIleSerGlnGlySerasnIleA 568

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773 CTGTATGACAGGGCTTGGTCTGCTTTCCAGCGAAACAAGATGGCCGC 822
568 lavalmetHISglYleuGlyLeuLeuSerThGluSnlyMetAlaArg 584
823 ATAAAGATTGGCAGATATGGCGCACTCAAGACTATGCCGACGAC 872
585 lIaSnAspLeuAlaSpMetAlaGlnLeuLysAspTyrAlaAlaAla 601
873 CATCCGCGATTGGCGATCCCAAAACCCCAATGCCGACAGGATGAAG 922
601 alIeAtgAspTyrAlaValaGlnAsnProAsnAlaAlaGlnGlyIleGlu 618
923 CGCTCAGCAATATCTTTATGGCAGCCATCCCATCAAGGATGGAGCT 972
618 lavalSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGlyAla 634
973 GTCCGGGGAATAATAGGCTTGGGCGGATCCAGCAGCATCCGTCAAGG 1022
635 ValArgGlyLysTyrGlyLeuGlyGlyIleThAlaHisProIleLysAr 651
1023 GTCCGAGATGGCGCGATGCGATGCGGAAAGGAAATCCGCGTCAGCG 1072
651 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 668
1073 ACAATTTTGGCGATGGCGCATACGCCAAATACCCGTCCCTTACCATTC 1122
668 sPaSnPheAlaAspAlaAlaTyrAlaLysTyrProSerProTyrHisSer 684
1123 CGAAATATCGCTCAAACTTGGAGCAGCGTTACGCAAGAAACAACTCAC 1172
685 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleTh 701
1173 CTCCTACACGCTGCGCGCTCAAAACGCAAAATGTCAACTGCGACGAC 1222
701 rSerSerThValProProSerAsnGlyLysAsnValLysIleAlaAspG 718
1223 AACGCCACCGAGAGACAGCGCTACCGTTTGACGCTTAAAGGTTTCCGAA 1272
718 lnaArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 734
1273 TTTGAGAGCAGCTGAATATGATAGC 1299
735 PheGlnLysHisValLysTyrAspThr 743

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAE10038
seq_documentation_block:
ID AAE10038 standard; Protein: 751 AA.
XX
AC AAE10038;
XX
DT 29-NOV-2001 (first entry)
XX
DE N. meningitidis strain 2996 961c-ORF46.1 fusion protein.
XX
KW Heterologous expression; Neisserial protein; open reading frame; ORF;
KW 961c-ORF46.1 fusion protein.
XX
OS Neisseria meningitidis 2996.
XX
PN WO200164920-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00420.
XX
PR 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;
  Pizza M;

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XX WPI: 2001-557776/62.
DR N-PSDB: AAD17053.
XX
PT Heterologous expression for the expression of two or more Neisserial
XX proteins in fused state
XX
PS Claim 18; Page 30; 52pp; English.
XX
CC The present invention relates to a method for simultaneous heterologous
CC expression of two or more Neisserial proteins which are in a fused
CC state. The method is useful for simultaneous heterologous expression of
CC two or more Neisserial proteins. A protein that may be unstable or
CC poorly expressed on its own is assisted by adding a suitable hybrid
CC partner and commercial manufacture is simplified-only one expression and
CC purification need to be employed in order to produce two separately-
CC useful proteins. The present sequence is Neisseria meningitidis
CC (serogroup B, strain 2996) 961c-ORF46.1 (open reading frame) fusion
CC protein.
XX
SQ Sequence 751 AA;

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alignment_scores:
  Quality: 2111.00      Length: 409
  Ratio: 5.200          Gaps: 0
  Percent Similarity: 99.267      Percent Identity: 97.311

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alignment\_block:

US-09-303-518D-463 x AAE10038 ..

Align seg 1/1 to: AAE10038 from: 1 to: 751

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351 sPheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyGluLeuA 368
173 CCNAGCGCAAGCGCATATCGGATTGGGAACATACAAAGCCATCAGTTG 222
368 lAglnArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 384
223 GGCCACGTGATGATCAACAGCGCGCTGTGAGAAATATCGGCTCAT 272
|||||
365 GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTyrII 401
273 TGTCCGCTTTTCGATCAGGGGCAAAATTCATCCGCTTCGACAAC 322
|||||
401 eValArgPheSerAspHisGlyHisGlnValHisSerProPheAspSnH 418
323 ATGCGTCATTTCCGATTCAGACGAGCGGTAAGTCCCGTTGACGATTC 372
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418 lSAlaSerHisSerAspSerAspGlnAlaGlySerProValAspGlyPhe 434
373 AGCCTTACCGCATCCATTGGAGGATAGACACCATCCGCGCAGCG 422
|||||
435 SerLeuTyrArgGlnHisIleTyrAspGlyTyrGlnHisIleProAlaAspG 451
423 CTATGACGCGCCACAGGCGCGGCTATCCGCTCCCAAGGCGGAGG 472
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451 yTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 468
473 ATATATACAGCTACGACATAAAGCGTTGCCCAAAATATCCGCTCAAC 522
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468 sPleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 484
523 CTGACGACAGACCGGAGCAGCAACGCGTTCGCGAGCTTCCGCAAA 572
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485 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 501

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373 AGCCTTACCGCATCCATTGGGAGGATAGCAACACATCCGCGCAGCG 422  
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 473 YTYrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArg 490  
 473 ATATATACAGCTACGACATAAAGGCTTGGCCAAATATCCGCGCTCAC 522  
 490 SPLeuTyrSerTyrAspIleLysGlyValAlaGlnHisTyrLeuAsn 506  
 523 CTGACGACAAACCCGACAGCCGACAAACGCTTGGCCGCTTTCACAA 572  
 507 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHis 523  
 573 TGCCTGGCGCTATCTGACGACAGGAGTACGACGATTCACAAACGCGCA 622  
 523 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 540  
 623 CCGGATACAGCCCGGAGCTGGAGACAGATCGGGCAATGCGCGCGAGCTTC 672  
 540 hTrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaAlaGlnAlaPhe 556  
 673 AACGGACATGACAGATATCGTCAAAAACATCATCGCGCGCGAGAGAAAT 722  
 557 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyIu 573  
 723 TGTGCGGCGAGCGGATCGCGTGGAGGTATAGCGAAGCGCTCAAACTTG 772  
 573 eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIleA 590  
 773 CTGTCAATGACAGCGCTGGGTCTGCTTCCAGCGAAACAGATGGCGCGC 822  
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 607 IleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAla 623  
 873 CATCCGGATTTGGGAGTCCAAAACCCCAATGGCGCACAGGAGCATAGAG 922  
 623 aIleArgAspTyrAlaValGlnAsnProAsnAlaAlaGlnGlyIleGlu 640  
 923 CCTCAGCAATATCTTATGGCAGCCATCCCATCAAGGAGTGGAGCT 972  
 640 lValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGlyAla 656  
 973 GTCGCGGGAATATACGCTTGGGCGCATCAGCAGCATCTCTGCAAGG 1022  
 657 ValArgGlyTyrTyrGlyLeuGlyGlyIleThrAlaHisProIleLysAr 673  
 1023 GTGCGAGATGGCGGCGATGCGATGGCGAAGGAAATCCGCGCTCAGCG 1072  
 673 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 690  
 1073 ACAATTTTGGCGATGGCGCATACGCCAATACCGTCCCTTACGATTCC 1122  
 690 sPAsnPheAlaAspAlaIaIaTyrAlaLysTyrProSerProTyrHisSer 706  
 1123 CGAAATATCGCTCAAACTGGAGCAGCGTTAGGCAAAAGAAACATCAC 1172  
 707 ArgAsnIleArgSerAsnLeuGlnGlnArgTyrGlyLysGlnAsnIleThr 723  
 1173 CTCTCTAACCGTGGCGCGCTCAAAACGCAAAAATGTCAATGCGACAGC 1222  
 723 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 740  
 1223 AAGGCCACCGGAGACAGGCTTACCGTTGACGCTAAAGGTTTCCGAAAT 1272  
 740 lnaArgHisProLysThrGlyValAlaProPheAspIleLysGlyPheProAsn 756

1273 TTTCGAGACGACGTGAATATGATAGC 1299  
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 AC AAE10041:  
 XX  
 XX  
 DT 29-NOV-2001 (first entry)  
 XX  
 XX  
 DE N. meningitidis strain 2996 961cL-ORF46.1 fusion protein.  
 XX  
 KW Heterologous expression; Neisserial protein; open reading frame; ORF;  
 KM 961cL-ORF46.1 fusion protein.  
 XX  
 OS Neisseria meningitidis 2996.  
 XX  
 PN W0200164920-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-IB00420.  
 XX  
 PR 28-FEB-2000; 2000GB-0004695.  
 PR 13-NOV-2000; 2000GB-0027675.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PI  
 PI Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;  
 PI Pizsa M;  
 XX  
 DR WPI: 2001-557776/62.  
 DR N-PSDB: AAD17056.  
 XX  
 PT Heterologous expression for the expression of two or more Neisserial  
 PT proteins in fused state -  
 XX  
 PS Claim 18; Page 32-33; 52pp; English.  
 XX  
 CC The present invention relates to a method for simultaneous heterologous  
 CC expression of two or more Neisserial proteins which are in a fused  
 CC state. The method is useful for simultaneous heterologous expression of  
 CC two or more Neisserial proteins. A protein that may be unstable or  
 CC poorly expressed on its own is assisted by adding a suitable hybrid  
 CC partner and commercial manufacture is simplified-only one expression  
 CC purification need to be employed in order to produce two separately-  
 CC useful proteins. The present sequence is Neisseria meningitidis  
 CC (serogroup B, strain 2996) 961cL-ORF46.1 (open reading frame) fusion  
 CC protein.  
 XX  
 SO Sequence 765 AA;  
 XX  
 alignment\_scores:  
 . Quality: 2111.00 Length: 409  
 Ratio: 5.200 Gaps: 0  
 Percent Similarity: 99.267 Percent Identity: 97.311  
 alignment\_block:  
 US-09-303-518d-463 x AAE10041 ..  
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 73 TCAGATTTGGCAAAAGATCCCTTATCCGCGAGTTCGACCGTCAACA 122  
 357 SerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgGlnHi 373  
 123 TTTCGACCCGACGGGAATATACACCTATTTCGACGACAGGCGGAGCTTG 172  
 373 sPheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyGlnLeuA 390

```

173 CCNAGCGCAACGGCCATATCGATTGGGAAACATACAAAGCCATCAGTTG 222
174 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
390 laGLuYserGlyHisIleGlyLeuClYusIleGInserHisGInLeu 406
223 GGCACCTGATGATTCACAGCGCGCGTGAAGAAATATCGGCTACAT 272
224 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
407 gLYAsnLeuMetIleGInGInAlaIleLeYsGlyAsnIleGlyrII 423
273 TGTCGGCTTTCCGATCAGCGGCAAAATCCATTCGCGCTTCGACAAAC 322
274 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
423 eValAlpHeSerAspHisGlyHisGlyValHisSerProPheAspAsn 440
323 ATGCTACATTCGATTCGATTCGACAAAGCCGTTAGTCCGTTGACGATTC 372
324 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
440 lsaIaSerHisSerAspSerAspGluAlaIleYserProValAspGlyPhe 456
373 AGCCTTACCGCATCCATTGGAGCGGATACAAACCCATCCGCGCAGCG 422
374 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
457 SerLeuYrArGlyIleHisTrpAspGlyTYrGluHisHisProAlaAspG 473
423 CTATGACGGCGCAAGGGCGGCTATCCCGCTCCCAAAAGGCGAGGG 472
424 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
473 YTYrAspGlyProGInGlyGlyTYrProAlaProLYsGlyAlaGArGa 490
473 ATATATACAGCTACGACATAAAAGCGCTGCCCCAAATATCCGCTCAAC 522
474 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
490 spIeTYrSerTYrAspIleLeYsGlyValAlaGInAsnIleArGLeuAsn 506
523 CTGACCGCAACACCGCAGCAACCGGATCGCGCGCTTCACCA 572
524 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
507 LeuHisrAspAsnArGSerTrnGlyGlnArGLeuAlaAspArGpHeHisAs 523
573 TGCCGGCGCTATGCTGACCGCAAGAGTAGGCGACGATTCACCAAGCGCA 622
574 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
523 nAlaGlySerMetLeuThrGInGInGlyAlaGlyAspGlyPheLYsArGAlAr 540
623 CCCGATACAGCCCCGAGCTGGACAGATCGGGCAATGCCGCCGAAGCTTC 672
624 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
540 hrArGTYrSerProGInLeuAspArGSerGlyAsnAlaGInAlaPhe 556
673 AAGGCGCTCGCATATCGTCAAAACATCATCGGCGCGCAGAGAAAT 722
674 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
557 AsnGlyTrnAlaAspIleValIlyAsnIleIleGlyAlaAlaGlyIuII 573
723 TGTCGGCGCAGGCGATGCCGTGACGGTATTAAGCGAAGGCTCAACATTTG 772
724 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
573 eValGlyAlaGlyAspAlaValGInGlyIleSerGInGlySerAsnIleA 590
773 CTGTCTATGCAGCGCTTGGTCTGCTTCCACGCAAAACAAGATGCGCGCG 822
774 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
590 lAValMetHisGlyLeuGlyLeuLeuSerThrGInAsnLYsMetAlaArG 606
823 ATCAAGATTGGCAGATATGGCGCAACTCAAGACTATGCGCGCACACAG 872
824 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
607 lIleAsnSPreUAlaAspMetAlaGInLeuLYsAspTYrAlaAlaAlaAl 623
873 CATCCGCGATTGGCAGTCCAAACCCCAATGCCGCAAGGATAGAG 922
874 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
623 AlleArGAspTYrAlaValGInAsnProAsnAlaAlaGInGlyIleGluA 640
923 CCCTCAGCAATATCTTTATGGCAGCCATCCCAAGGATGGAGCT 972
924 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
640 lAValSerAsnIlePheMetAlaAlaIleProIleLYsGlyIleGlyAla 656
973 GTCCGGGGAAAAATACGCTTGGCGGCATCAGCGCATCTCTGTCAGCG 1022
974 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
657 ValArGglyLYsTYrGlyLeuGInGlyIleTrnAlaHisProIleLYsAr 673
1023 GTCCGAGATGGGCGCATTCGCGCAAGGAAATCCGCGCTCAGCG 1072
1024 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
673 gSerGInMetGlyAlaIleAlaLeuProLYsGlyLYsSerAlaValSerA 690

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1073 ACAATTTTGGCGATGCGGCATACGCCAAATACCCGCTCCCTTACCATTC 1122
1074 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
690 sPAsnPhelAlaAspAlaAlaIlyrAlaLYsTYrProSerProTYrHisSer 706
1123 CGAAATATTCGTTCAACTTGGAGCAGCGTTTACGGCAAAAGAAACATCAC 1172
1124 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
707 ArGAsnIleArGSerAsnLeuGInGInArGTYrGlyLYsGInAsnIleTh 723
1173 CTCTCAACCGCGCGCGCTCAACGCGAAATGTCAACTCGCAGACC 1222
1174 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
723 rSerSerThrValProProSerAsnGlyLYsAsnValLYsLeuAlaAspG 740
1223 AACGCCACCGCAAGACAGCGCTACCGTTTGACGGTAAAGGCTTCCGAT 1272
1224 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 lArGHisProLYsThrGlyAlaProPheAspGlyLYsGlyPheProAsn 756
1273 TTTGAGAAAGCACGTGAATATGATACG 1299
1274 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
757 PheGInLYsHisValLYsTYrAspThr 765
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seq_documentation_block:
ID AAU27600 standard; Protein: 806 AA.
AC AAU27600;
XX
AC AAU27600;
XX
DT 18-DEC-2001 (first entry)
XX
DE Neisseria meningitidis fusion protein 961-ORF46.1.
XX
XX Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
KW Neisserial protein.
XX
OS Neisseria meningitidis.
XX
XX Synthetic.
XX
PN WO200164922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00452.
XX
PR 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Maignani V, Gulliani MM,
PI Pizsa M;
XX
DR WPI; 2001-582163/65.
XX
DR N-PSDB; AAS43897.
XX
PT Producing heterologous proteins from Neisseria meningitidis and N.
PT gonorrhoeae -
XX
PS
XX
XX Example 23; Page 67; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisserial proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 806 AA;

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    ratio: 5.200    gaps: 0  
 Percent Similarity: 99.267                      Percent Identity: 97.311

alignment\_block:  
 US-09-303-518D-463 x AAU27600 ..

Align seg 1/1 to: AAU27600 from: 1 to: 806

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73  TCAGATTGGCAAAACGATCCCTTATCCGCGAGCTTCTGACCCGTACGA 122.
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123  TTTCGAACCCGACGCGGAATATACCATTCCTGGCAGAGGGGGAGCTTG 172
|||||
406  spheGluProAspGlyLysTyrHisLeuPheGlySerArgGlyGlnLeuA 423
173  CCNAGCCGAAGGCGCATATCGATTGGGAAACATACAAAGCCATCAGTTG 222
|||||
423  laGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 439
223  GGGCACTGATGATTCACACAGGCGCGCTTGAAGAAATATCGCGCTACAT 272
|||||
440  GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTyrIle 456
273  TGTCCGCTTTCCGATCACGCGGCAAAATTCATTCGCCCTTGACACAC 322
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456  eValArgPheSerHisSglYHisGlnValHisSerProPheAspAsnH 473
323  ATGCTTCACATTCGATTTCTGACGAAGCGGATGCTCCGTTGACGATTC 372
|||||
473  IsAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 489
373  AGCCTTTACCGCATTCATGGGAGCGATACGAACACATCCGCGCAGCG 422
|||||
490  SerLeuTyrArgIleHisThrPaspGlyTyrGlnHisIleProAlaAsp 506
423  CTATGACGGGCGCACAGGGCGGCGCTATCCGCTCCCAAGGCGCGAGG 472
|||||
506  yTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 523
473  ATATATACAGCTACGACATAAAAGCGCTTGCCTCCCAATATCCGCTCAAC 522
|||||
523  spIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 539
523  CTGACCGACAAACCGCAGACCGGACAAAGGCTTCCGACCGCTTCCACA 572
|||||
540  LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 556
573  TGGCGGCGGTATGCTGACGCAAGAGTAGCGAGGATTCAAAGCGCGCA 622
|||||
556  naIaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 573
623  CCGGATACAGCCCCCGAGCTGGACAGATCGGCAATCGCGCGAAGCCTTC 672
|||||
573  hrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIaGlnAlaPhe 589
673  AACGCGACTGCAGATATCGTCAAAAACATCATCGGCGCGGAGGAAT 722
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590  AsnGlyThrAlaAspIleValIlysAsnIleIleGlyAlaIaIaGlyGln 606
723  TGTGGCGCAGGCGATCCGTCAGGCTATTAAGCAAGGCTCAACATTTG 772
|||||
606  eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIleA 623
773  CAGTCATGACAGGCTTGGCTGCTTCCACCGAAACAAAGTGGCGCGC 822
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623  laValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 639
823  ATCAACGATTTGGCAGATATGGCGCAACTCAAGACTATGCGCGAGCAGC 872
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873  CATCCGCGATTGGCAGTCCAAACCCCAATGCCGACAGGATACAG 922
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656  alIeArgAspTyrPAlaValGlnAsnProAsnAlaIaGlnIleGlyIleG 673
923  CCGTCAGCAATATCTTTATAGCAGCATCCCATCCATCAAGGATGGAGCT 972
|||||
673  laValSerAsnIlePheMetAlaIaIaIleProIleLysGlyIleGlyAla 689
973  GTCCGGGGGAAATACGCTTGGGCGGCATACAGGACATCTGTCCACG 1022
|||||
690  ValArgGlyLysTyrGlyLeuGlyLysIleThrAlaHisProIleLysAr 706
1023  GTCCGAGATGGGCGGATCGCATTCGCCAAGGGAATCCCGCTACAGC 1072
|||||
706  gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 723
1073  ACAATTTTCCGATCGGCATACGCCAAATACCCGCTCCCTTACCATTC 1122
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723  spAsnPheAlaAspAlaIaIaTyrAlaLysTyrProSerProTyrHisSer 739
1123  CGAAATATCCGTTCAACTTGAGCAGCGTTACGGCAAAAGAAACATCAC 1172
|||||
740  ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleTh 756
1173  CTCCCAACCCGCGCGCGTCAACAGGCAAAATGTCAAACTGCGCAGCC 1222
|||||
756  rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaSpG 773
1223  AACGCCACCCGCAAGACAGCGCTTACCGTTGACGGTAAAGGTTCCGAT 1272
|||||
773  lNArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 789
1273  TTTGAGAAGCACGTGAATATGATACG 1299
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790  PheGlnLysHisValLysTyrAspThr 798

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AC  AAE10035;
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DT  29-NOV-2001 (first entry)
XX
DE  N. meningitidis strain 2996 961-ORF46.1 fusion protein.
XX
KW  Heterologous expression; Neisserial protein; open reading frame; ORF;
KW  961-ORF46.1 fusion protein.
XX
OS  Neisseria meningitidis 2996.
XX
PN  WO200164920-A2.
XX
PD  07-SEP-2001.
XX
PF  28-FEB-2001; 2001MC-IB00420.
XX
PR  28-FEB-2000; 2000GB-0004695.
PR  13-NOV-2000; 2000GB-0027675.
XX
PA  (CHIR-) CHIRON SPA.
XX
PI  Arico MB, Comanducci M, Galeotti C, Masignani V, Giuliani MM,
PI  Pizza M;
XX
DR  MPI; 2001-557776/62.
XX
N-PSDB; AAD17050.
XX
PT  Heterologous expression for the expression of two or more Neisserial
XX  proteins in fused state

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PF 09-OCT-1998: 98WO-IB01665.  
 XX  
 PR 01-SEP-1998: 98GB-0019016.  
 PR 06-NOV-1997: 97GB-0023516.  
 PR 14-NOV-1997: 97GB-0024190.  
 PR 18-NOV-1997: 97GB-0024386.  
 PR 27-NOV-1997: 97GB-0025158.  
 PR 10-DEC-1997: 97GB-0026147.  
 PR 14-JAN-1998: 98GB-0000759.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PI Grandi G, Masignani V, Pizza M, Rappoli R, Scarlato V;  
 XX WPI, 1999-327407/27.  
 DR  
 XX Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for  
 PT diagnosis, treatment and prevention of infection  
 XX  
 PS Claim 4: Page 274; 524pp; English.  
 XX  
 CC Amino acid sequences AA138499-138944 represent *Neisseria meningitidis*  
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open  
 CC reading frames (ORFs) AA11972-212358. The antigenic proteins,  
 CC their fragments, their nucleic acids and antibodies are used for  
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*  
 CC infections, such as meningitis, septicemia and gonorrhea. Both  
 CC organisms are closely related. Fragments of the nucleic acids  
 CC are useful as hybridisation probes and antisense reagents.  
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 US-09-303-518D-463 x AAY38729 ..

Align seg 1/1 to: AAY38729 from: 1 to: 298

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17 gLySGlnAspGlyAlaHisGlnArgPheGlyArgTyrGlyAlaThrGlnA 34
856 GACATATGCCGACAGCGCATCCGCGATTTGGCGAGTCCAAACCCCAATGC 905
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34 gLyLeuCysArgSerSerHisProArgLeuGlySerProLysProGlnCys 50
906 CGCACAAGGATAGAACCCGTCAGCAATATCTTTATGGCAGCCATCCCA 955
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51 ArgThrArgHisArgSerArgGlnGlnTyrLeuTyrGlySerHisProH 67
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67 sGlnArgAspTyrSerCysProGlyLysIleGlnLeuGlyArgHisHisG 84
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|||||
84 LysThrSerCysArgAlaValAlaAsp**ArgAspArgIleCysGlnArg 100
1056 GAAATCGCGCGTCAGCACAATTTTGGCGATGGCGCATACGCCAATATCC 1105
|||||
101 GlnIleArgArgGlnArgGln**CysArgCysArgLeuGlyLysIlePr 117
1106 CGTCCCTTACATTCGCCAATATTCGTTCAAACTTGAGCAGACGCTTAC 1155
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149 nValLysLeuAlaAspGlnArgHisProLysThrGlyValProPheAspG 166
1256 GTAAGGGTTTCCGAATTTTGAGAACGACGTGAAATATGATACGAGCTC 1305
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1456 ACTAGTCATTTAAAGCCCATCGGCAACGAGATGCGAAATGAAATACACG 1505
|||||
233 SerSerGlnPheLysAlaHisAlaGlnArgGlnTyrPheGlnAsnLysThrGln 249
1506 GTTAGATTTTAAATCATTTTATAGTGTGATGATATCAATTAAGAAAGCAGACG 1555
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1556 TAACAGAGGCGCATAGTCTAACCCGCTGATGTACGGGTGATACACAA 1605
|||||
266 aThrGlyGlyHisSerLeuThrArgGlyAspValArgValIleGlnGln 282
1606 ACCTGGGACGCTGATTAACATGAGGT..TTATCAACGACGACGCAAT 1652
|||||
283 ThrSerAlaProAspLysHisGlyValLeuSerSerAspSerGlyAsn 298
seq_name: /SIDS1/9cgcdata/geneseq/geneseq-emb1/AA1999.DAT: AAY38728
seq_documentation_block:
ID AAY38728 standard; Protein: 227 AA.
XX
XX AAY38728;
AC
XX
XX 08-OCT-1999 (first entry)
DT
XX
DE Neisseria meningitidis antigen encoded by a partial ORF46.
KW
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
XX Neisseria meningitidis.
OS
XX
XX W09924578-A2.
PN
XX
XX 20-MAY-1999.
PD
XX
XX 09-OCT-1998: 98WO-IB01665.
PF
XX
XX 01-SEP-1998: 98GB-0019016.
XX 06-NOV-1997: 97GB-0023516.
XX 14-NOV-1997: 97GB-0024190.
XX 18-NOV-1997: 97GB-0024386.
XX 27-NOV-1997: 97GB-0025158.
XX 10-DEC-1997: 97GB-0026147.
XX 14-JAN-1998: 98GB-0000759.
XX
XX (CHIR-) CHIRON SPA.

```

XX Grandi G, Masiagnani V, Pizze M, Rappuoli R, Scarlato V;  
 PI WPI: 1999-327407/27.  
 XX DR N-PSDB; AA212172.  
 XX PT Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for  
 PT diagnosis, treatment and prevention of infection  
 XX  
 PS Claim 4; Page 274; 524pp; English.  
 CC Amino acid sequences AA18499-18494 represent *Neisseria meningitidis*  
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open  
 CC reading frames (ORFs) AA211972-212358. The antigenic proteins,  
 CC their fragments, their nucleic acids and antibodies are used for  
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*  
 CC infections, such as meningitis, septicaemia and gonorrhoea. Both  
 CC organisms are closely related. Fragments of the nucleic acids  
 CC are useful as hybridisation probes and antisense reagents.  
 CC  
 SQ Sequence 227 AA;

alignment\_scores:  
 Quality: 1163.00 Length: 227\*  
 Ratio: 5.215 Gaps: 0  
 Percent Similarity: 98.238 Percent Identity: 94.714

alignment\_block:  
 US-09-303-518d-463 x AAY38728 ..

Align seg 1/1 to: AAY38728 from: 1 to: 227

43 GCACTGTCCTCGCATGCGATGCGATTCGATTCGCAACGATCC 92  
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 1 AAlaValcysLeuProMetHisAlaHisAlaSer\*\*LeuAlaAsnAspSe 17  
 93 CTTTATCCGCGAGGTTCTCGACGCTGACATTCGATTCGACCGGGAAT 142  
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 17 rPheIleArgIleValIleuAspArgIleHisPheGluProAspGlyIst 34  
 143 ACCACCTATTCGCGACGAGGGGAGCTTCGCNAGCGCAAGGCCATATC 192  
 |||||||  
 34 yHisIleuPheGlySerArgGlyIleuIleuIleuIleuIleuIleu 50  
 193 GGATTGGAAACATACAAAGCATGATGGCGCACTGATGATTCACA 242  
 |||||||  
 51 GlyLeuGlyIleGlnSerHisGlnLeuGlyAsnLeuMetIleGlnI 67  
 243 GCGCGCCGTTGAAAGAAATATCGGCTACATTCGCTTCGATCAGC 292  
 |||||||  
 67 nAlaIleIleuGlyAsnIleGlyIleValArgPheSerAspIstG 84  
 293 GGCACAAATTCATTCGCTTCGACACCATGCTTCATTCGATTCCT 342  
 |||||||  
 84 lYHisGlnValIleHisSerProPheAspAsnHisAlaSerHisSer 100  
 343 GACGAACCGGTAGTCCGTTGAGCGATTCAGCTTACCGCATTCAT 392  
 |||||||  
 101 AspGlnIleGlySerProValAspGlyPheSerLeuIleHisIst 117  
 393 GGACGATATGACACCATCCCGCGAGGCTATGACGGCCACAGGGCG 442  
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 117 paspGlyTyrGlnHisIstProIleAspGlyTyrAspGlyProGlnI 134  
 443 GCGGCTATCCCGCTCCAAAGCGCGAGGATATATACAGCTACGACA 492  
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 134 lYgIlyTyrProIleAspGlyIleValArgPheIstIleTyrSerTyr 150  
 493 AAAGCGCTTGCGCAAAATATCCGCTTCACCTGACCGGACGAGGAC 542  
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 151 LysGlyValAlaGlnAsnIleArgLeuAsnLeuThrAspAsnArgSer 167

543 CGGACAAACGCTTCCGACCGCTTCCACATTCGCGCGCTATGTCAGC 592  
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 167 rGlyGlnArgLeuAlaAspArgPheHisAsnIleGlySerMetLeuTrnG 184  
 593 AAGGATGAGCGACGATTCAAACGCGCCACCGCATACAGCCCGAGCTG 642  
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 184 lGlyValGlyAspGlyPheIstArgAlaThrArgTyrSerProIleu 200  
 643 GACAGATCGGCAATGCGCGAGCGCTTCACAGGCGACGACATATCGT 692  
 |||||||  
 201 AspArgSerGlyAsnAlaIleuAlaIleuAlaPheAsnGlyThrAlaAsp 217  
 693 CAATAACATCATCGCGCGCGAGGAGAAATT 723  
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 217 lYsAsnIleIleGlyAlaAlaGlyIle 227  
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 XX  
 AC AAY75498;  
 XX  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE *Neisseria gonorrhoeae* ORF 730 protein sequence SEQ ID NO:2470.  
 XX  
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
 KW antibacterial; gene therapy.  
 XX  
 OS *Neisseria gonorrhoeae*.  
 XX  
 PN W0957280-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US09346.  
 XX  
 PR 01-MAY-1998; 98US-0083758.  
 PR 31-JUL-1998; 98US-0094869.  
 PR 02-SEP-1998; 98US-0098994.  
 PR 02-SEP-1998; 98US-0099062.  
 PR 09-OCT-1998; 98US-0103749.  
 PR 09-OCT-1998; 98US-0103794.  
 PR 09-OCT-1998; 98US-0103796.  
 PR 25-FEB-1999; 99US-0121528.  
 PR  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masiagnani V, Mora M;  
 PI Petersen J, Pizze M, Rappuoli R, Ratti G, Scarlato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 XX  
 DR WPI: 2000-062150/05.  
 DR N-PSDB; AA254260.  
 XX  
 PT Novel *Neisseria* polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics  
 XX  
 PS Claim 2; Page 1181; 1453pp; English.  
 XX  
 CC AA53015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941  
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the  
 CC presence of *Neisseria* bacteria, or to raise antibodies. They may also



```

          :::::::::::
499 HislaInglInArgLysGluGluAlaLysAnAspSerHisArgSerVa 515
1503 AGGGTTGATTTAATCATTTTATAGTGGTGAATCAATAAAGGCA 1552
515 IGLY...AspSerAnArgValAlaArgGluGlyLysGlnTyrLeuAspS 531
1553 CAGTAACAGAGGAGCATAGTCTTAACCGGTGATGATGAGGATACAA 1602
531 erAspThrGlyAsnHisValTyrValLysGlyAspLysValIle... 546
1603 CAAACCTCGGCACCTGATTAACATGGGGTTTATCAA..... 1638
547 .....LeuThrProAspGlyArgGlnValThrGlnPheLysAnSerLy 561
1639 .GGCAGACGTGGAAATTAAGCCTGATGGAAGTTGGAGAGTCAA 1683
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seq_name: /sids1/gcgdata/geneseq/geneseq-emb1/AA25499
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ID   AAY75499 standard; Protein; 467 AA.
XX
XX   AAY75499;
XX
XX   21-MAR-2000 (first entry)
XX
XX   Neisseria meningitidis ORF 730 protein sequence SEQ ID NO:2472.
XX
XX   Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX   antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
XX   antibacterial; gene therapy.
XX
XX   Neisseria meningitidis.
XX
XX   WO957280-A2.
XX
XX   11-NOV-1999.
XX
XX   30-APR-1999; 99WO-US09346.
XX
XX   01-MAY-1998; 98US-0083758.
XX   31-JUL-1998; 98US-0094869.
XX   02-SEP-1998; 98US-0098964.
XX   02-SEP-1998; 98US-0099062.
XX   09-OCT-1998; 98US-0103749.
XX   09-OCT-1998; 98US-0103794.
XX   09-OCT-1998; 98US-0103796.
XX   25-FEB-1999; 99US-0121528.
XX
XX   (CHIR) CHIRON CORP.
XX   (GENO-) INST GENOMIC RES.
XX
XX   Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M,
XX   Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
XX   Tettelin H, Venter JC;
XX
XX   WPI: 2000-062150/05.
XX   N-PSDB: AA54261.
XX
XX   Novel Neisserial polypeptides predicted to be useful antigens for
XX   vaccines and diagnostics -
XX
XX   Claim 2; Page 1182; 1453pp; English.
XX
XX   AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
XX   represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
XX   and polypeptides. AA254537 to AA254576 and AA254616 to AA254473 represent
XX   PCR primers used in the exemplification of the present invention. The
XX   polypeptides, the polynucleotides, antibodies and compositions of
XX   the invention can be used as vaccines, as diagnostic reagents, and as
XX   immunogenic compositions. The polypeptides can be used in the

```

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CC   manufacture of medicaments for treating or preventing infection due to
CC   Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC   presence of Neisseria bacteria, or to raise antibodies. They may also
CC   be used to screen for agonists or antagonists, which may themselves
CC   have use as antibacterial agents. The polynucleotides of the invention
CC   may also be used in gene therapy protocols.
XX
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XX   Alignment scores:
XX       Quality: 752.50      Length: 511
XX       Ratio: 2.280        Gaps: 11
XX   Percent Similarity: 64.579   Percent Identity: 34.247
XX
XX   alignment_block:
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XX
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5 ArgArgLeuThrAsnLeuAlaAlaAcysAlaValAlaAlaAlaAla 21
54 GCCGATGCATGCACAGCCCTCAGATTGGCAAGATCCCTTATCCGC 103
   |:::| | | | | | | | | | | | | | | | | | | | |
21 uileGlnProAlaLeuAlaAlaAspLeuAlaGlnAspProheleThra 38
104 AGCTTCTGACCCGTCAGATTTCGACCCGACGGGAATACCACCTATTC 153
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38 spAsnAlaGlnArgGlnHisTyrGluProGlyGlyLysTyrHisLeuPhe 54
154 GGCAGC...AGGGGGAGCTTGCACCAAGCGCCATCCGAGATTGGG 200
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55 GlyAspProArgGlySerValSerAspArgThrGlyLysIleAsnValI 71
201 AAACATACAAGCCATCAGTTGGCCACCTGATTCACAGGCGCCG 250
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71 eGlnAspTyrThrHisGlnMetGlyAsnLeuLeuileGlnGlnAlaAsnI 88
251 TTGAAGGAATATGCGCTACATTCGTCGCTTTCGATCAGCGGCACAA 300
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||
88 IeAsnGlyThrIleGlyTyrHisThrArgPheSerGlyHisGlyHisGlu 104
301 TTCATTCGCCCCCTTCGACACACAGCCCTCAGATTCCGATTCGACGAAGC 350
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105 GlnHisAlaProPheAspAsnHisAlaAlaAspSerAlaSerGluGly 121
351 CGGTAGTCCCGTTGACGATTCAGCCCTTACCGCATCCATTGGACGAGAT 400
   |||:|:| | | | | | | | | | | | | | | | | | |
121 sGlyAsnValAspArgGluGlyPheThrValArgLeuAsnTrpLeuGln 138
401 ACGACACACATCCCGCGCAGCGCTATGACGGCGCAGCGGGGGCGAT 450
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||
138 IsgLinhHisProAlaAspAlaTyrAspGlyProLysGlyLysAsnYr 154
451 CCCGCTCCCAAGCGCGCAGGATATATACAGCTACGACAAAGAGCGT 500
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155 ProLysProThrGlnGlyAlaArgAspGlyThrThrTyrHisValAsnGlyTh 171
501 TGCCCAAAATATCCGCTCAACCTGACCGACACCGCAGCAGCGACAC 550
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171 rAlaArgSerIleLysLeuAsnProThrAspThrArgSerIleArgGlnA 188
551 GCGTTGCCGACCGCTTTCACATGCCGCGCTATGCTGACCGCAAGAGSTA 600
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188 rGlnSerAspAsnTyrIserAsnLeuGlySerAsnPheSerAspArgAla 204
601 GCGCGAGATTCAAAGCGCGCAGCATCAGCCCGCGGACAGATC 650
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651 GGGCAATCGCGCGAAGCCTTCAACGGCATGACAGATATCGTCAAAAACA 700

```



```

55 GlyAspProArgGlySerValSerAspArgThrGlyLysIleAsnValI 71
201 AAGCATATCAAGAGCATGAGTTGGCCAGCATGATTCATCAAGCGCGCG 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 eGlnAspTyrThrHisGlnMetCysLysLeuLeuIleGlnGlnIleAsn 88
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 TTGAAGAAATATCGGCTACATTCGCTTTCCGATACGGCGGCACAA 300
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351 CGGTAGCCCGGTTCGACGATTCGCTTACCGCATTCATGGGACGAGT 400
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121 sGlyAsnValAspGlyGlyPheThrValTyrArgLeuAsnTrpGlyGln 138
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138 IsgLysHisProIleAspAlaTyrAspGlyProLysGlyLysAsnTyr 154
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451 CCGGCTCCCAAGGCGCGAGGATATATACAGCTACGACATAAAGCGT 500
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155 ProLysProThrGlyAlaArgAspGlyTyrThrTyrHisValAsnGly 171
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171 rAlaArgSerIleLysLeuAsnProThrAspThrArgSerIleArgGln 188
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188 rGlyLeuSerAspAsnTyrSerAsnLeuGlySerAsnPheSerAspArg 204
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205 AspGlnAlaAsnArgGlyMetPheGlnHisAsnAlaLysLeuAsnArg 221
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651 GGGCAATGCGCGCGAGCCTTCACAGCGACCTGACGATATCGTCAAAACA 700
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221 pGlyAsnSerMetClnPheIleAsnGlyValAlaAlaGlyAlaLeuAsn 238
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255 ThrArgTyrAlaIleAspLysAlaIleAsnArgAsnIleAlaProLeu 271
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801 CACCGAAACAGATGCGCGCATCAACGATTCGCGATATGCGCGCAAC 850
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271 oAlaGlnGlyLysPheAlaValIleGlyLysLeuGlySerValAlaGly 288
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851 TCAAGAGCTATGCCGACGACCATCCGCGATTCGCGCAAAACCC 900
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288 heGlyLysAsnThrArgGlnAlaValAlaAspArgTrpIleGlnGlnAsn 304
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901 AATGCGCGCAAGGATAGAGCGCTCAGCAATATCTTATGCGACCCAT 950
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305 AsnAlaIleGlnThrValGlnAlaValAlaPheAsnValAlaAlaAla 320
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951 CCCATCAAGGATTCGAGCTTCGCGGAAATACGGCTTCGCGGCGCA 1000
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320 ..... 320
1001 TCACGGACATCTGTCAGCGGTCGACAGATGGCGCGCATTCGATTCG 1050
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321 .....LysValAlaLysLeuAlaLysAlaAlaLysPro 331
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1051 AAGGGAATCCGCGCTCAGCGCAATTTTCGCGATCGCGCATCCGCCAA 1100
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332 ...GlyLysAlaIleValSerGlyAspPheAlaAspSerTyrLysLys 347
    : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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1101 ATACCCGTCCTTACCATTCGCCAAATATCGTTCAACTGTGAGCAGC 1150
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347 sLeuAlaLeuSerAspSerAlaArgGlnLeuTyrGlnAsnAlaLysTyr 364
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
1151 GTTACGGCAAGAAACATCATCTCTCAACCGTCGCGCGCTCAACGCC 1200
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
364 rG.....GluAla 366
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
1201 AAAAATGTCAACAGTGGCAGCCAGCCAGCCGAGACAGCGGCTT 1250
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
367 LeuAspIleHisTyrGlnAspLeuIleArgArgLysThr..... 379
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380 AspGlySerSer.....LysPheIleAsnG 388
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1301 AGCTGATATTCAGAAATTCGCGGGCGGTATACCTAAGGCTAAGCCT 1350
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388 LysArgGlnIleAspAlaValThrAsnAspAlaLeuIleGlnAlaLysArg 404
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seq_documentation_block:
ID AAV75500 standard; Protein; 498 AA.
XX
AC AAV75500;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 730 protein sequence SEQ ID NO:2474.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN W0957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99MO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

```

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 DR WPT, 2000-062150/05.  
 DR N-PSDB: AA254262.

XX Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics  
 PS Claim 2: Page 1183; 1453pp; English.

XX AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941  
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC *Neisseria* bacteria (e.g. meningitis and septicemia), to detect the  
 CC presence of *Neisseria* bacteria, or to raise antibodies. They may also  
 CC be used to screen for agonists or antagonists, which may themselves  
 CC have use as antibacterial agents. The polynucleotides of the invention  
 CC may also be used in gene therapy protocols.

SO Sequence 498 AA:

alignment\_scores:  
 Quality: 740.50 Length: 586  
 Ratio: 2.165 Gaps: 18  
 Percent Similarity: 58.362 Percent Identity: 32.253

alignment\_block:  
 US-09-303-518D-463 x AA275500 ..

Align seg 1/1 to: AA275500 from: 1 to: 498

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28 ATCTGTGTCATCTGCGAGTGTG.....CTGCCGAT 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 LeuLeuLeuLeuLeuAlaAlaCysAlaValAlaAlaAlaLeuLeuIle 23
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 GCATGCGACGCGCTGATTTGGCAAGCATCCCTTATCCGCGAGTTC 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
23 nProAlaLeuAlaAlaAspLeuAlaGlnAspProPheIleThrAspAsn 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
110 TCGACGCTGACATTTGGAACCGGCGGAATACACATATTCGCGAGC 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 IagIaArgIaInIstArgIaProIaGlyIaTyIaInIstLeuPheIaAsp 56
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160 ...AGGGGAGAGCTTGGCCNAGCGGACGCGCATTCGATTTGGAAACAT 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 ProIaArgIaSerIaValSerAspArgThrIaGlnIleAsnValIleGlnAs 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 ACAAGACATCAGTTGGGCCACGATGATTAACAGCGCGCTGAG 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 pTyIaThrIaArgMetIaGlnLeuLeuIleGlnIaAlaAsnIleAsnG 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
257 GAAATATCGCTACATTTGCGCTTTTCGATCGACGGGCAAAATTCAT 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
90 IyIaThrIleGlyIaTyIaInIstArgPheSerGlyIaTyIaGlnIaInIst 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 TCGGCTTTCGACACATGCTTCATTCGATTCGACGAGCGGCTAG 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 AlaProPheAspAsnIaAlaAlaAspSerAlaSerIaGlnIaTyIaGlyAs 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
357 TCCGCTGACGATTCAGCTTTACCGCATTCATTTGGACGAGTAACAAC 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
123 nValAspGlnIaGlyPheThrIaValIaTyIaArgLeuAsnIleIaGlnIaIn 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
407 ACATTCGCGCGGACGCTATGACGGGCGACAGGGCGGCTATCCGCT 456
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140 IStIaSProAlaAspAlaIaTyIaAspIaProIaGlyIaAsnTyIaProIa 156

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457 CCCAAAGCGGCGGATATATACAGTACGACATAAAGCGTTGCCA 506
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157 ProThrGlyAlaIaArgAspGlyIaTyIaThrIaIstValaInIaGlyIaThrAla 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 AAATATCGCGCTCAACCTGACGACACACCGACGCGGACGCGCTTG 556
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
173 gSerIleIaLeuAsnProIaThrArgSerIleArgIaGlnIaGlyIa 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
557 CCGACCGTTTCACAATCGCGGCTATGCTGACCAAGAGTATGGCAC 606
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 eAspAsnTyIaSerIaInIaGlySerIaAsnPheSerAspArgAlaAspIu 206
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607 GATTCAAAGCGGCGACCGCATACAGCCCGCGCTGACATCGCGGCA 656
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 AlaAsnIaGlyIaMetPheGlnIaIstAsnIaIaIaLeuAsnIaPheGlyAs 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
657 TCCGCGCGAAGCTTCAACGCGCATCTGACATATGTCAAAACATCATCG 706
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
223 nSerMetGluPheIleAsnGlyValAlaIaGlyAlaLeuAsnProPheI 240
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707 GCGCGGACGAGAAATTTGCGCGGCGCATCCGCTCAGGCTATTAAC 756
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240 IeSerAlaGlyIaGlnIaLeuGlyIaGlyIaAspIleIaTyIaGlyIaThrArg 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
757 GAAGGCTCAACATTCGTGTCAATGCGAGGCTTGGCTGCTCCACCGCA 806
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
257 TyIaAlaIleAspIaValaIaMetArgAsnIleAlaProIaProIaIaG 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
807 AAACAAGATGCGCGCATCAACGATTTGGCAGATATGGCGCACTCAAG 856
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 nGlyIaSPheAlaValIleGlyIaGlyLeuGlySerValaIaGlyIaPheGlyIu 290
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
857 ACTATGCGCGACGACATCCGCGATTTGGGACGTCCAAACCCCAATGC 906
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290 yAsnThrArgIaGlnIaValaIaAspArgIaIleGlnIaAsnProIaAla 306
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907 GCACAAGCATAGAACGCGTCAGCAATATCTTATGCGACGCCATCCCAT 956
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 AlaGluThrValGlnIaLeuValaIaAsnValaIaLeuProIaPheAla 320
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957 CAAGGATTTGAGCGTTCGCGGGAATATCGCTTGGCGCGCATCACGG 1006
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320 ..... 320
1007 CACATCTCTCAAGCGGTGCGAGATGGCGCGATGCGATGCGCGAAAGG 1056
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 .....LysValIaIaAsnLeuThrIaValaIaIaLysPro...Gly 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1057 AAATCGCGCGTCAAGCGACAAATTTGGCGGATGCGCATACGCCAAATATACC 1106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
333 IyAlaAlaValaIaSerIaIaSPheSerAlaAla..... 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1107 GTCCCTTACCATTCGCGAATATCGCTTCAAACTTGGACGAGCGCTAG 1156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
344 .....TyIaAsnThrArgThrIaArgIaValIaThrIaGlnIaGly 358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1157 GCAAAGAAACATCACCTCTCAACCGTGCAGCGCTCAACAGGCAAAAT 1206
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358 IyLeuAsnArgIleArg.....GlnAsnIaIaLysAsn 368
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1207 GTCAACCTGCGACGACCGACCGCGCGAAGACAGCGGTACCGTTGACGG 1256
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369 SerAsnIleIaGlnIaLysAsnTyIa.....Gly 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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377 yArgAspAsnProAsn.....HisIleAsnValaIaLeuSerGlyAsn 391
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1307 ATATTCAAGAAATTA.....TCGGGGGCGGCTATACCTAAG 1341
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391 eIleGlnIaIstIleLeuTyIaGlyAspGlnIaGlyIaGly..... 404

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1342 GCTAAGCCTGTGTTGATGCGAAACG.....AG 1370
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1371 ATGGAGCTGATAGAGAGCTTAAATGACAACTCGAGACAGTGG 1420
      ::|||
419 sTrpSerAla.....SerLysIleThr..... 426
1421 AGAAATGTTTCAGAAACGAGAAAGACAGTACAGTACGTTTAA 1470
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427 .....HisLulIleSerAlaPleVal 433
1471 GCCCATGCGCAACGAGATGGGAAATTAACAGGCTTACATTATCA 1520
      ::|||
434 ThrSerProLysThrGlnTrpLysAlaGlnThrGly..... 445
1521 TTTTATAGTGTGATATCAATAGAAAGCAGATACAGAGGCGCAT 1570
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446 .....ThrGlyGlyLysT 450
1571 GTCTAACCCGTGTGATGTACGGGTATACAAACCTCGCACCTGAT 1620
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450 yrlLeuAlaLysGly.....ArgProAlaArgTrpValSerTyrluThr 464
1621 AACATGCGGTTTATCAACGACAGTGGAAATTAACAGCTGATGAAG 1670
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465 ArgAspLylLeuArgLysThrVal..... 473
1671 TTGGGAGGTGAAACGAAAGAGTGGAAAGTATGACCAACGACCA 1720
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474 .TyrluProAlaThr.....GlyLysValVal.....Thra 484
1721 TGTTCCTCA 1728
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484 LaphPro 486

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seq_documentation_block:
ID AU27596 standard; Protein: 353 AA.
XX
AC AU27596;
XX
DT 18-DEC-2001 (first entry)
XX
DE Fusion protein 730-C2 containing IS5 insertion sequence.
XX
KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX
KW Neisserial protein.
XX
OS Neisseria meningitidis.
XX
OS Escherichia coli.
XX
PN WO20016922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00452.
XX
PR 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Massignani V, Guillani MM;
PI Piza M;
XX
WP1: 2001-582163/65.
XX
DR Producing heterologous proteins from Neisseria meningitidis and N.
XX
PT gonorrhoeae -
XX
PS Example 21; Page 61; 119pp; English.

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XX
CC The invention relates to methods for the heterologous expression of
CC Neisserial proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AU27553-AU27610 represent Neisserial proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 353 AA:

alignment_scores:
      Quality: 725.50      Length: 370
      Ratio: 2.834      Gaps: 4
Percent Similarity: 69.189      Percent Identity: 40.811

alignment_block:
US-09-303-518D-463 x AU27596 ..

Align seg 1/1 to: AU27596 from: 1 to: 353

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123 TTTCGACCCGAGCGGAAATACACACTATTCGGGAGC...AGGGGGAGC 169
   ::|||
18 sTyrluProGlyLysTyrluHisLeuPheGlyAspProArgLyserv 35
170 TTGCGMCGCGACAGCGCATATTCGGATTGGAAACATACAAAGCCATCAG 219
   ::|||
35 aISerAspArgThrGlyLysIleAsnValIleGlnAspTyrluHisGln 51
220 TTGGGCGACCTGATGATTCACACAGCGCGCTGAAGAAATATCGGCTA 269
   ::|||
52 MetGlyAsnLeuLeuIleGlnGlnAlaAsnIleAsnLysThrIleGly 68
270 CATGTCCGCTTTCCGATCCAGGCGCACAAATTCGATCCGCTTCGACA 319
   ::|||
68 rHisThrArgPheSerGlyHisGlnIleGlnAlaIleAlaProPheAsp 85
85 snHisAlaAlaAspSerAlaSerGlnIleLysGlyAsnValAspGly 101
370 TTCAGCCCTTACCGCATTCGAGGAGATAGCAACACCATCCGCGCGCA 419
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102 PheThrValTyrluArgLeuAsnTrpGlnGlyHisGlnHisProAlaAs 118
420 CGGCTATGACGGGCGCACAGGCGGCGGTATCCCGTCCGAAAGCGCGCA 469
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118 PalatyrAspGlyProLysGlyLysAsnTyrluProLysProThrGlyAla 135
470 GGGATATATACAGCTACGACATAAAGCGTGGCCCAATATCCGCTC 519
   ::|||
135 rGAspGlyTyrluThrTyrluHisValAsnGlyThrAlaArgSerIleLys 151
520 AACCTGACGCGACAGCGACGCGGCGGTTCGACCGGCTTCGCA 569
   ::|||
152 AsnProThrAspTrpArgSerIleArgGlnArgIleSerAspAsnTyrlu 168
570 CAATGCGCGGCTATGCTGACGAGAGAGTAGCGCAGATTCAAAGCGC 619
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168 rAsnLeuGlySerAsnPheSerAspArgAlaAspGlyAlaAsnArgLys 185
620 CCACCGCATACAGCCCGAGCTGGACAGATGCGCAATGCGCGGAGAC 669
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185 etPheGlnHisAsnAlaLysLeuAspArgTrpGlyAsnSerMetGluPhe 201

```



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570 CAATGCCGGCGGCGATGCTGACGCAAGAGCTGAGCGACGGATTCAACACCG 619
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168 rfsnleuglyserasnpheneseraspargalaaspdlunlaasnarglysm 185
    ::::: ::::: ::::: ::::: ::::: :::::
620 CCACCCGATACGACCCCGAGCTGAGCACATGCGCAATGCGCGCAAGCC 669
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185 eepheglnuhsnlnalalsysleuaspargtpglyasnsermetcluphe 201-
    ::::: ::::: ::::: ::::: ::::: :::::
670 TTCACGGCATCTGCAGATATCGTCAAAAACATCATCGCGCGGAGAGAGA 719
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202 llaasnlglyalaialaaglyalaleuasnprophelieseralaglygl 218
    ::::: ::::: ::::: ::::: ::::: :::::
720 AATTGGCGCGGAGCGGATGCCGCTGACGGTAAAGRTAAAGCAAGCTCAACA 769
    ||| ||||| ||||| ||||| ||||| |||||
218 lalaenuglylileglyaspilieleutyrglythyrargtyrlaalleasp 235
    ||| ||||| ||||| ||||| ||||| |||||
770 TTGCTGTCTATCGACGCGTTGGGTGCTGTTTCACCGCAAAACATAGATGGC 819
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
235 ysalaalame tar ysnllea laa proleuproalaglueglylyspheala 251
    ::::: ::::: ::::: ::::: ::::: :::::
820 CCGATCAACGATTTGGCAGATATGGCGACMACTCAAGACATATGCGCGAGC 869
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
252 ValileglylyleuglyserValaialaaglyheglulysantrhrargl 268
    ::::: ::::: ::::: ::::: ::::: :::::
870 AACCATCCCGCGATTGGGCAGTCCAAACCCCAATCCGCGCACAGCATAg 919
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
268 uLaValaaspargtpPileglnuasnprohsnalalaaglythrValag 285
    ||||| ||||| ||||| ||||| ||||| |||||
920 AAGCGGTGACGAATATCTTTATGGCAGCGCATCCCATCAAGAAGGATTGGA 969
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285 lLaValaLphehsnValaLaLaLaLaLaLaLaLaLaLaLaLaLaLaLaLa 294
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970 GCTGTCCGGGAAAAATACGCGCTGGCGCATCGCACATCCTCTGCAA 1019
    |||
295 .....Ly 295
    .....
1020 GCGGTCCGAGATGGCGCGCATTCGCGAAAGGAATCCGCGCTCA 1069
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295 sValaLaLysleuLaLaLysLaLaLaLysPro...GlyLysLaLaLaValaLs 311
    ::::: ::::: ::::: ::::: ::::: :::::
1070 GGCAGAAATTTGGCGATCGCGCATACGCCAAATATCCGCTCCCTTACCAT 1119
    || ::::: ||||| ::::: |||
311 eeglyAspPheLaAspserTyrIysLysLysLeuLaLaLeuSerAspSer 327
    ::::: ::::: ::::: ::::: ::::: :::::
1120 TCCCGAAATATCCGTTGAGACCTTGAGCAGCGCT 1152
    ::::: ::::: ::::: ::::: ::::: :::::
328 AlaArgInleuTyrGlnAsnAlaLysTyrArg 338
    ::::: ::::: ::::: ::::: ::::: :::::
seq_name: /SITS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: AAB37856
seq_documentation_block:
ID AAB37856 standard; Peptide; 125 AA.
AC AAB37856;
XX
XX
DT 26-FEB-2001 (first entry)
XX
XX Neisserial conserved peptide #39.
XX
XX DE Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;
XX KW gene therapy; conserved sequence.
XX
XX OS Neisseria sp.
XX
XX PN WC020006741-A2.
XX
XX PD 09-NOV-2000.
XX
XX PF 28-APR-2000; 2000MO-IB00642.
XX
XX PR 30-APR-1999; 99GB-0010168.
XX PR 09-MAR-2000; 2000GB-0005128.
XX
XX

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PA (CHIR-) CHIRON SPA.  
XX  
PI Rappunoli R;  
XX  
DR WPI: 2000-687543/67.  
XX  
PT Novel Neisserial protein fragments and their corresponding nucleic  
PT acids, useful in the manufacture of medicines for the prevention of  
PT Neisserial infection, and in the manufacture of diagnostic reagents -  
PS  
XX  
PS Claim 15; Page 58; 157pp; English.  
XX  
XX The present peptide is a conserved region of a Neisserial protein.  
CC Neisserial proteins containing this sequence, and the nucleic acids  
CC that encode such proteins, are useful in the manufacture of medicines  
CC for the prevention of Neisserial infection, and in the manufacture of  
CC multi-specific diagnostic reagents.  
XX  
XX Sequence 125 AA;  
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[illegible]

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US-09-303-518D-463 x AAB37856 ..
Align seg 1/1 to: AAB37856 from: 1 to: 125
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XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen: vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;  
 KW antibacterial; gene therapy.  
 OS Neisseria gonorrhoeae.  
 PN WO957280-A2.  
 PD 11-NOV-1999.  
 PF 30-APR-1999; 99WO-US09346.  
 PR 01-MAY-1998; 98US-0083758.  
 PR 31-JUL-1998; 98US-0094869.  
 PR 02-SEP-1998; 98US-0098994.  
 PR 02-SEP-1998; 98US-0099062.  
 PR 09-OCT-1998; 98US-0103749.  
 PR 09-OCT-1998; 98US-0103794.  
 PR 09-OCT-1998; 98US-0103796.  
 PR 25-FEB-1999; 99US-0121528.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 DR WPI: 2000-062150/05.  
 DR N-PSDB; AA254162.  
 PT Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics  
 PS Claim 2; Page 1101; 1453pp; English.  
 XX AA253015 to AA254536, AA254577 to AA254615, and AA254253 to AA25941  
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the  
 CC presence of Neisseria bacteria, or to raise antibodies. They may also  
 CC be used to screen for agonists or antagonists, which may themselves  
 CC have use as antibacterial agents. The polynucleotides of the invention  
 CC may also be used in gene therapy protocols.  
 XX  
 XX Sequence 131 AA.  
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     Ratio: 5.015  
     Gaps: 0  
 Percent Similarity: 100.000      Percent Identity: 100.000  
 alignment\_block:  
 US-09-303-518D-463/rev x AA254400 ..  
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 17 IGtGtlyPheGlyIleAlaArgSerValGlnLeuGlyAlaValSerG 34  
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 seq\_documentation\_block:  
 ID AA254402 standard; Protein: 131 AA.  
 AC AA254402;  
 DT 21-MAR-2000 (first entry)  
 XX Neisseria meningitidis ORF 686 protein sequence SEQ ID NO:2278.  
 DE  
 XX  
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;  
 KW antibacterial; gene therapy.  
 OS Neisseria meningitidis.  
 PN WO957280-A2.  
 PD 11-NOV-1999.  
 PF 30-APR-1999; 99WO-US09346.  
 PR 01-MAY-1998; 98US-0083758.  
 PR 31-JUL-1998; 98US-0094869.  
 PR 02-SEP-1998; 98US-0098994.  
 PR 02-SEP-1998; 98US-0099062.  
 PR 09-OCT-1998; 98US-0103749.  
 PR 09-OCT-1998; 98US-0103794.  
 PR 09-OCT-1998; 98US-0103796.  
 PR 25-FEB-1999; 99US-0121528.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 DR WPI: 2000-062150/05.  
 DR N-PSDB; AA254164.  
 PT Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics  
 PS Claim 2; Page 1101-1102; 1453pp; English.  
 XX AA253015 to AA254536, AA254577 to AA254615, and AA254253 to AA25941  
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent

PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the presence of *Neisseria* bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.

Sequence 131 AA:

alignment\_scores:

Quality: 636.00 Length: 131  
Ratio: 4.892 Gaps: 0  
Percent Similarity: 99.237 Percent Identity: 96.183

alignment\_block:

US-09-303-518D-463/rev x AAY75402

Align seg 1/1 to: AAY75402 from: 1 to: 131

```

723 AATTCTCTCGCCGCGCGATGATCTTTTGAAGATATCGATCCGCT 674
|||||
1 Asnphesercysarvalaspaspvalpneaspapilcysseralava 17
673 TGAAGGCTTCGGCGGATGCCGATCTGTCAGCTCGGGGCTGTATCG 624
|||||
17 Lguserpneglylylealargservalglneuglyalavalaserg 34
623 GTGCGCGCTTTGAATCCGTCGCTACTCCTGCGTCAGATAGCGCGGC 574
|||||
34 Lylalaphnegluservalalatyserleuarglinitshrtrrgly 50
573 ATTGTGGAACGGTCGCGCAAGCCGTTGTCGGTGCCTGTCGTCGTC 524
|||||
51 lilevalglthrvalasplysproleuserglyalalavalalgllyc 67
523 GGTTCGAGGCGAATTTGGGCAAGCCCTTTATGTCGTAGCTATATA 474
|||||
67 nvalglualalaspilaleuglyasnalaheryvalalavalalyti 84
473 TCCCTGCGCCCTTTGGAGCGGAGATAGCCGCGCCCTGTGCGCGTAT 424
|||||
84 lproarvalaphneglyserglylealalalaleutrrprovalille 100
423 GCGGTGCGCGGATGCTGTTGCTATCCGCCAATGATGCGGTAAAGGC 374
|||||
101 Alalavalgllylmetvalphevalsevalprometaspalavallysai 117
373 TGAATCGTCACGAGGACTACCGGCTTGTGCAATCGGAATG 331
|||||
117 agluservalasnnglythrthrlylphenlearglileglymet 131

```

seq.name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: AAY75401

seq\_documentation\_block:

ID AAY75401 standard; Protein: 163 AA.

AAV75401:

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 686 protein sequence SEQ ID NO:2276.

Neisseria meningitidis: *Neisseria gonorrhoeae*; antigen; vaccine;

antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

antibacterial; gene therapy.

Neisseria meningitidis.

PN WO957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-0509346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUL-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 25-FEB-1999; 99US-0121528.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;

XX Petersen J, Piza M, Rappoli R, Ratti G, Scalato E, Scarselli M;

XX Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX N-PSDB; AA254163.

XX Novel *Neisseria* polypeptides predicted to be useful antigens for

XX vaccines and diagnostics

XX Claim 2; Page 1101; 1453pp; English.

XX AA253015 to AA254536, AA254577 to AA254615, and AA254253 to AA25941

XX represent novel *Neisseria* meningitidis and *N. gonorrhoeae* polynucleotides

XX and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent

XX PCR primers used in the exemplification of the present invention. The

XX polypeptides, the polynucleotides, antibodies and compositions of

XX the invention can be used as vaccines, as diagnostic reagents, and as

XX immunogenic compositions. The polypeptides can be used in the

XX manufacture of medicaments for treating or preventing infection due to

XX *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the

XX presence of *Neisseria* bacteria, or to raise antibodies. They may also

XX be used to screen for agonists or antagonists, which may themselves

XX have use as antibacterial agents. The polynucleotides of the invention

XX may also be used in gene therapy protocols.

XX Sequence 163 AA:

alignment\_scores:

Quality: 636.00 Length: 137  
Ratio: 4.782 Gaps: 0  
Percent Similarity: 97.080 Percent Identity: 91.971

alignment\_block:

US-09-303-518D-463/rev x AAY75401

Align seg 1/1 to: AAY75401 from: 1 to: 163

```

741 GGCATCGCGCTGCGCGACAAATTCCTCGCGCGCGATGTTTGA 692
|||
27 GYAla*****Asnphesercysserlaspaspvalpneas 43
691 CGATATCTGACGATGCGGTTGAAGGCTTCGCGGATGCGCGATCTGTC 642
|||||
43 naspilcysserlavalalugluphneglyglylealalargservalg 60
641 AGCTCGGGGCTGTATCGGGTGGCGGCTTTGAATCGCTGCTACTCTCT 592
|||||
60 lneuglyalavalserglylylaphnegluservalalatyserleu 76
591 CGTCAGATAGCGCGCGCATTTGGAAGCGTGGCAAGCGCTTGTTCGG 542
|||||
77 Arglnhishthrthrlylvalglutthrvalgllylserleu 93

```

541 TCGTCGGCTGTCGTCAGTGTAGCGGATATTTGGGCAACGCTTTT 492  
|||||  
93 yAlaAlaValAlaValGlnValGlnAlaAspIleuGlyAsnAlaPheT 110  
491 ATGTCGAGCTGATATATCCCTCGCGCTTCGAGCGGATAGCGGCC 442  
|||||  
110 yValValAlaValAlaValTyrIleProAlaPheGlySerIleAlaAla 126  
441 GCCCTTGCGCCGTCATAGCCGTCGCGGAGTGTGTCATCCGCTCC 392  
|||||  
127 AlaLeuTyrProValIleAlaValGlyGlyMetValPheValSerValPr 143  
391 AATGATGCGGTAAAGCTGATCGCTCAACGGAGCTACCGGCTTCGCA 342  
|||||  
143 OmEtaSPAlaValIlyAlaIlySerValAsnGlyThrThrGlyPheIleA 160  
341 GAATCGAATG 331  
160 rGileGlyMet 163

seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AA37857

seq\_documentation\_block:

ID AAB37857 standard; Peptide: 119 AA.

AC AAB37857;

DT 26-FEB-2001 (first entry)

DE Neisserial conserved peptide #40.

KM Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

KW gene therapy; conserved sequence.

OS Neisseria sp.

PN WO20066741-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-IB00642.

PR 30-APR-1999; 99GB-0010168.

PR 09-MAR-2000; 2000GB-0005728.

PA (CHIR-) CHIRON SPA.

PI Rappuoli R;

DR WPI: 2000-687543/67.

PT Novel Neisserial protein fragments and their corresponding nucleic

PT acids, useful in the manufacture of medicines for the prevention of

PT Neisserial infection, and in the manufacture of diagnostic reagents -

PS Claim 15; Page 58; 157pp; English.

CC The present peptide is a conserved region of a Neisserial protein.

CC Neisserial proteins containing this sequence, and the nucleic acids

CC that encode such proteins, are useful in the manufacture of medicines

CC for the prevention of Neisserial infection, and in the manufacture of

CC multi-specific diagnostic reagents.

SO Sequence 119 AA;

alignment\_scores:

Quality: 595.00

Ratio: 5.000

Percent Similarity: 100.000

Length: 119

Gaps: 0

Percent Identity: 100.000

alignment\_block:

US-09-303-518D-463 x AAB37857 ..

Align seg 1/1 to: AAB37857 from: 1 to: 119

583 ATGTCGAGCAAGAGATGAGCGAGATTCAAAGCGCCACCGATACAG 632  
|||||  
1 MetLeuThrGlnGlyValGlyAspGlyPheIlySerAlaThrAlaGlyTyrSe 17  
633 CCCCGAGCTGGACAGATCGGGCAATGCCCGCAAGCCTTCACGCGCATG 682  
|||||  
17 rProclunEuAspArgSerGlyAsnAlaIleAlaGlnAlaPheAsnGlyThrA 34  
683 CAGATATGCTCAAAACATCATCGCGCGGCAAGAAATTTGTCGGCGCA 732  
|||||  
34 IaAspIleValIlyAsnIleIleGlyAlaAlaGlyGlnIleValGlyAla 50  
733 GCGCATGCGCGTGCAGGTATTAAGCAGAGCTCAACATTCGTCATGCA 782  
|||||  
51 GlyAspAlaValAlaGlnGlyIleSerGlnGlySerAsnIleAlaValMetHl 67  
783 CGGCTTGGGTCCTTTCACCGAAGAACAGATGCGCGCATCAACGATT 832  
|||||  
67 sGlyLeuGlyLeuLeuSerThrGlnAsnIlyMetAlaArgIleAsnAspL 84  
833 TGGCAGATATGCGGCACTCAAGACTATGCCGACAGCATCCGCGAT 882  
|||||  
84 euAlaAspMetAlaGlnLeuIlyAspTyrAlaAlaAlaIleAlaIleArgasp 100  
883 TGGCGAGTCGCAAAACCCGATGCCGACAGCAGCAGATAGAGCGCTCAGCA 932  
|||||  
101 TyrAlaValAlaGlnAsnProAsnAlaAlaGlnGlyIleGlnAlaValSerAs 117  
933 TATCTTT 939  
|||||  
117 nIlePhe 119

seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:AA38727

seq\_documentation\_block:

ID AAY38727 standard; Protein: 127 AA.

AC AAY38727;

DT 08-OCT-1999 (first entry)

DE Neisseria meningitidis antigen encoded by a partial ORF46.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.

OS Neisseria meningitidis.

PN WO9924578-A2.

PD 20-MAY-1999.

PF 09-OCT-1998; 98WO-IB01665.

PR 01-SEP-1998; 98GB-0019016.

PR 06-NOV-1997; 97GB-0023516.

PR 14-NOV-1997; 97GB-0024190.

PR 18-NOV-1997; 97GB-0024386.

PR 27-NOV-1997; 97GB-0025158.

PR 10-DEC-1997; 97GB-0026147.

PR 14-JAN-1998; 98GB-0000759.

PA (CHIR-) CHIRON SPA.

PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;

DR WPI: 1999-327407/27.

DR N-PSDB; AA21217L.

PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

PT diagnosis, treatment and prevention of infection  
 XX  
 PS Claim 4; Page 273; 524pp; English.  
 XX

CC Amino acid sequences AA538499-Y38944 represent *Neisseria meningitidis*  
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open  
 CC reading frames (ORFs) AA21972-212358. The antigenic proteins,  
 CC their fragments, their nucleic acids and antibodies are used for  
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*  
 CC infections, such as meningitis, septicemia and gonorrhea. Both  
 CC organisms are closely related. Fragments of the nucleic acids  
 CC are useful as hybridisation probes and antisense reagents.  
 XX  
 SO Sequence 127 AA:

alignment\_scores:  
 Quality: 560.00 Length: 125  
 Ratio: 4.786 Gaps: 0  
 Percent Similarity: 93.600 Percent Identity: 89.600

alignment\_block:  
 US-09-303-518D-463 x AA538727 ..

Align seg 1/1 to: AA538727 from: 1 to: 127

```

1279 AAGCAGCTGAATATGATACGAGCTCGATTTATTCAGAAATATTCGGGGG 1328
      ::::::::::::::: |||
2   GlnTyrValGlnPheSerIleAspLeuPheSerValGlyLysSerGly 18
1329 CGGTATACCTAAGGCTAAGCTGTGTGTTAGTGGAAACCGAGATGGAGG 1378
      |||
18   yGlyIlePhePolysAlaLysProValPheAspAlaLysProArgTyrGlu 35
1379 TTGTATGGAAGCTTATTAATTGACACACGCGAGAGCTGGAGAAAT 1428
      |||
35   aAspArgLysLeuAsnLysLeuThrThrArgGlnGlnValGlyLysAsn 51
1429 GTTCAGGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1478
      |||
52   ValGlnGluThrArgArgArgSerGlnSerSerGlnPheLysAlaHis 68
1479 GCACAGAGATGGGAAATTAACAGAGGTTAGATTTTAACTTTTANAG 1528
      |||
68   aGlnArgGluTyrGluAsnLysThrGlyLeuAspPheAsnHisPheIle 85
1529 GTGGTATATTCATTAAGAAAGCAGCAGTAAAGAGGAGGATGCTTAAC 1578
      |||
85   LysLysPheLeuAsnLysLysGlyThrValThrGlyLysHisSerLeuThr 101
1579 CGTGTGATGTACGGGTGATACAAACCTCGCAGCCTGATTAACATGG 1628
      |||
102   ArgGlyAspValAlaArgValIleGlnGlnThrSerAlaProAspLysHis 118
1629 GGT.TTATCAAGCGACATGGAAT 1652
      | |||
118   y**LeuSerSerAspSerGlyAsn 126

```

seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AA574707

seq\_documentation\_block:

ID AA574707 standard; Protein: 498 AA.

XX AA574707;

XX 21-MAR-2000 (first entry)

XX *Neisseria gonorrhoeae* ORF 238 protein sequence SEQ ID NO:888.

XX *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;  
 XX antibacterial; gene therapy.

OS *Neisseria gonorrhoeae*.

XX WO9957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUN-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 25-FEB-1999; 99US-0121528.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

XX Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalzo E, Scarselli M;

XX Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX N-PDB; AA253469.

XX Novel *Neisseria* polypeptides predicted to be useful antigens for

XX vaccines and diagnostics

XX Claim 2; Page 544; 1453pp; English.

XX AA253015 to AA254536, AA254577 to AA254615, and AA574253 to AA575941  
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254773 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of  
 CC the invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the  
 CC manufacture of medicaments for treating or preventing infection due to  
 CC *Neisseria* bacteria (e.g. meningitis and septicemia), to detect the  
 CC presence of *Neisseria* bacteria, or to raise antibodies. They may also  
 CC be used to screen for agonists or antagonists, which may themselves  
 CC have use as antibacterial agents. The polynucleotides of the invention  
 CC may also be used in gene therapy protocols.

SO Sequence 498 AA:

alignment\_scores:  
 Quality: 453.00 Length: 427  
 Ratio: 1.834 Gaps: 18  
 Percent Similarity: 57.845 Percent Identity: 31.616

alignment\_block:  
 US-09-303-518D-463 x AA574707 ..

Align seg 1/1 to: AA574707 from: 1 to: 498

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19   ATATCCCTTATTCGTCCATACGAGTGCCTGCGATGCAT..... 63
      |||
5   IleGlnLysPheMetLeuMetLeuAlaAlaAlaIleSerMetAspHis 21
64   .....GCACAGCGCTCAGATTGGCAACAGATCCCTTATTCGGCAGG 106
      ::|||
21   eProIleSerHisAlaAsnGlyLeu.....AspAlaArgLeuArgAsp 36
107   TTTCGACCGCTCAGCATTTGCAACCGCAGGGAATATTCAGCTATTCGGC 156
      ::|||
36   spMetGlnAlaLysHisTyrGluProGlyLysTyrHisLeuPheGly 52
157   ...AGCAGGGGGAGCTTGCCTGCGCAACGCGCATATTCGATTGGGAAA 203
      ::|||

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53 AsnAlaArgGlySerVal.....LysAsnArgValCysAlaValAlaGlnTh 67
204 CATCAAGAGCATCAGTGGGCACTGATG.....ATTCAACAGG 244
67 rPheAspAlaThrAlaValGlyProIleLeuProIleThrHisGluArgT 84
245 CGGCGCTTGAAGAAATATCGCTACATTCGCGCTTTTCGATCAAGG 294
84 hrcIyPheGluGlyValIleGlyTYrGluThrHisPheSerGlyHisGly 100
295 CACAAATTCATTCGCGCTTTCGACAACATGCTCACAATTCGATTCGA 344
101 HisGluValHisSerProPheAspHisAspSerLysSerThrSerAs 117
345 CGAAGCGCGATGTCGCTGACGATTCACGCTTACCGCATTCATGGG 394
117 pPheSerGlyGlyValAspGlyGlyPheThrValTYrGlnLeuHisArgT 134
395 ACGGATACGACACATCCCGCGAGCTATGACGCGGCGACAGGCGCG 444
134 hrcIySerGluIleHisProAlaAspGlyTYrAspGlyProGlnGly 150
445 GGGTATCCCGCTCCCAAGGCGGAGGATATATACAGCTACGACATAA 494
151 GlyTYrProGluProGlnGlyAlaArgAspIleTYrSerTYrHisIle 167
495 AGGCGTTGCCCAATATTCGCTCAAC..... 522
167 sGlyThrSerThrLysThrLysIleAsnThrValProGlnAlaProPheS 184
523 .....CTGACCGACACCGGACGACGCGACGCGCTTGGCGAG 561
184 eArgspArgTrpLeuLysGluAsnAlaGlyAlaAlaSerGlyPheLeuSer 200
562 CGTTTCCACAATCCGCGCTATGCTGACGCAAGAGTAGCGAGCGATT 611
201 ArgAlaAspGluAlaGlyLysIleTrpGluAsnAspProAspLysAs 217
612 CAACCGCGCCGCGATACAGCCCGAGCTGACAGATCGGCGAATCGCG 661
217 nTrpArgAlaAsnArgMetAsp.....AspIleArgGlyIleValG 251
662 CCGAAGCGCTCAAGGCGACTGACAGATGCTCAAAAACATCAACGCGG 711
231 IlnGlyAlaValAsn.....ProPheLeuThrGlyPhe 241
712 GCAGAGAAATTCGCGCGCA.....GGCGATCCGTCGAGGGATTAAG 755
242 GlnGlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValTh 258
756 CGAAGGCTCAACATTCGCTCATGCACGCG.....TTGGGCTGCG 796
258 rAspThrAlaAlaGlnIlnThrLeuGlnGlyIleAsnAspLeuGlyAsnL 275
797 TTTCACCGCAAAACAGATGGCGCATCAAGATTGGCAGATTAAGCG 846
275 euserProGluAlaGlnLeuAlaAlaAlaSerLeuGlnAspSerAla 291
847 ...CAACTCAAGACTATGCGCGACGACGATCCGCGATTGGCGACTCA 893
292 PheAlaValLysAspGlyIleAsnSerAla...ArgIlnTrpAlaAspAl 307
894 AAACCCCAAT.....GCCGCAAAAGGATGAAGCCG 925
307 aHisProAsnIleThrAlaThrAlaGlnThrAlaLeuAlaValAlaGlu 323
926 TCACCAATATCTTATGCGACGATCCCATCAAGGAGATGGAGCTGTC 975
324 AlaAlaGlyThrValTrpArg.....GlyLysLysValGluLeuAs 337
976 CGGGGAAATACGGCTTGGCG.....GCAT 1001
337 nProThrLysTrpAspTrpValLysAsnThrGlyTYrLysLysProAla 354

```

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1002 CACGCGACATC.....CTGTCAACGCGTCCGAGATGG 1033
354 lAArgHisMetGlnThrValAspGlyGluMetAlaGlyGlyAsnArgPro 370
1034 GCGCGATCGCATTCGCCAAGAGAAATCCCGCTACGACGACATTTGGCC 1083
371 ProLysSerIleThrSerGluGlyLysAlaAsnAlaIleThrTYr.... 385
1084 GATGCGGATACGCCCAATATACCGCTCCCTTACCATTCGCCAATATCCG 1133
386 .....ProLysLeuValAsnGlnLeuAsnG 394
1134 TTCAACTTGGAGCGCTTACGCGCAAG 1162
394 lGlnAsnLeuAsnAlaIleAlaGln 403
seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AAV38584
seq_documentation_block:
ID AAV38584 standard; Protein; 498 AA.
XX
AC AAV38584;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria gonorrhoeae antigen encoded by ORF29.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria gonorrhoeae.
XX
PN W09924578-A2.
XX
PD 20-MAY-1999.
XX
PE 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI: 1999-32407/27.
XX
DR N-PSDB; AA212046.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PS diagnosis, treatment and prevention of infection.
PS Claim 4; Page 146-147; 524pp; English.
XX
CC Amino acid sequences AAV38499-138944 represent Neisseria meningitidis
CC and N. gonorrhoeae antigenic proteins. They are encoded by open
CC reading frames (ORFs) AA211972-212358. The antigenic proteins,
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of Neisseria
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX
SQ Sequence 498 AA;

```

```

alignment_scores:
Quality: 452.00      Length: 427

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Ratio: 1.823 Gaps: 19  
Percent Similarity: 58.080 Percent Identity: 31.850

alignment\_block:  
US-09-303-518D-463 x AAY38584

Align seg 1/1 to: AAY38584 from: 1 to: 498

```

19 ATATCCCTTATTTCTGTCATCTGTCAGTGTGCTGCGATG...CAT...63
||||| : : : : : ||||| : : : : : ||| |||
5 IleGlnLysPheMetIleuLeuAlaIleSerMetIleuHis1 21
64 .....GCACACGCTCAAGATTGGCAACAATCCCTTATTCGGCAGG 106
||||| : : : : : |||
21 eProlIeSerHisAlaAsnArgLeu.....AspAlaArgLeuArgAspA 36
107 TTCTGCGCGCTGAGCATTTGCAACGCGAGGAAATACCACTATTCGGC 156
: : : : : ||||| : : : : : ||||| : : : : : |||||
36 sPheIeGlnAlaLysHisTyrGlnProGlyLysTyrHisLeuPheGly 52
157 ...AGCAGGGGGAGCTTGCSCNAGCGCAACGCGCATTCGATTCGGAA 203
: : : : : ||||| : : : : : ||||| : : : : : |||||
53 AsnAlaArgLysSerVal.....LysAsnArgValCysAlaValGlnTh 67
204 CATACAAAGCATCACTTGGCGCCACTGATG.....ATTCACACG 244
: : : : : ||||| : : : : : ||||| : : : : : |||||
67 rPheAspAlaThrAlaValAlGlyProIleLeuProlIeThrHisGluArgT 84
245 CGGCGCTTGAGGAATATCGGCTCATTCGCGCTTTCGATTCAGCGG 294
: : : : : ||||| : : : : : ||||| : : : : : |||||
84 hEiLysPheGlnGlyValIleGlyTyrGlnThrHisPheSerIleHisGly 100
295 CACAAATTCATTCGCGCTTGCACAAACATGCTCATTCGATTCGATTCGA 344
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
101 HisGlnValHisSerProPheAspHisSerLysSerThrSerHis 117
345 CGAAGCGGTAGTCCGCTGTCAGGATTCAGCTTACCGCATTCATTCGAG 394
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
117 rPheSerIleGlyValAspGlyLysPheThrValTyrGlnLeuHisArgT 134
395 AGGATACGACACATCCGCGCGGCTATGAGCGGCGACAGGCGGCG 444
||| ||| ||||| : : : : : ||||| : : : : : |||||
134 hGlySerIleIleHisProIleAspGlyTyrAspGlyProIleGly 150
445 GGCTATCCCGCTCCCAAGCGCGAGGATATATACAGTACAGATTA 494
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
151 GlyTyrProGlnProGlnIleAlaArgAspIleTyrSerTyrHisIle 167
495 AGGCGTGGCCCAAAATATCCGCTCAAC.....522
||||| : : : : : |||
167 sGlyThrSerThrLysThrLysIleAsnThrValProGlnAlaProPhe 184
523 .....CTGACCGCACACCGCAGCAGCGCAACGCGTTCGCGAC 561
||| : : : : : ||||| : : : : : ||||| : : : : : |||||
184 eTAspArgTrpLeuLysGlnAsnAlaGlyAlaIleSerGlyPheLeuSer 200
562 CGTTTCCACATGCGCGGCTATGCTGACGCAAGGATAGCGGATTC 611
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
201 ArgAlaAspGlnAlaGlyLysLeuIleTrpGlnAsnAspProAspLys 217
612 CAAAGCGCGCACCGCATACAGCGCGGAGTGCAGATCGGCAATGCCG 661
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
217 nTTrpArgAlaAsnArgMetAsp.....AspIleArgGlyIleValG 231
662 CGGAGCCCTTCAACGCGACATGATATGTCAAAACATCATTCGCGCG 711
||| ||| : : : : : ||||| : : : : : ||||| : : : : : |||||
231 hGlyAlaValAsn.....ProPheLeuThrGlyPhe 241
712 GCAGAGAAATTTGCGCGCA.....GCGATGCGCTGACGAGTATTAAG 755
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
242 GlnGlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValTh 258
756 CGAAGGTCACAAACATTTGCTGTCATCAGCGC.....TTGGGTCTGC 796

```

```

258 RAspThrAlaIleGlnGlnThrLeuGlnGlyIleAsnAspLeuLysnL 275
: : : : : ||||| : : : : : ||||| : : : : : |||||
797 TTTCACCGCAAAACAAGATGGCGCGCATCAACGATTTGGCAGATATGCG 846
||||| ||| : : : : : ||||| : : : : : ||||| : : : : : |||||
275 eUSePProGlnAlaGlnLeuAlaIleSerLeuLeuGlnAspSerAla 291
847 ...CAACTCAAGACTATGCGCGCAGACGCGATCCGCGATTCGGCAGTCCA 893
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
292 PheAlaValLysAspGlyIleAsnSerAla...ArgGlnThrAlaAspAl 307
894 AAACCCCAAT.....GCCGCAACAGGATGACAGCCG 925
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
307 hISProAsnIleThrAlaThrAlaGlnThrAlaLeuAlaValAlaGln 323
926 TCAGCATATTCATTATGCGACCCATCCCATCAAGAGGATTCGAGCTGTC 975
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
324 AlaIleGlyThrValITrPArg.....GlyLysLysValGlnLeuAs 337
976 CGGGGAAATATCGGCTTGGCGG.....GCAT 1001
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
337 nProThrLysTrpAspTrpValLysAsnThrGlyTyrLysLysProAla 354
1002 CACGCGCACATC.....CTGTCAAGCGGTCCGAGATGG 1033
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
354 IaArgHisMetGlnThrValAspGlyGlnMetAlaGlyLysAsnArgPro 370
1034 CGCGGATGCGATTCCGCAAGGAAATCCGCGCGTACCGCATTTTGGC 1083
: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
371 ProlYSerIleThrSerGlnGlyLysAlaAsnAlaIleThrTyr..... 385
1084 GATCGCGCATATCGGCAAAATACCGCTCCCTTACCATTCGCGAAATATCCG 1133
||| : : : : : ||||| : : : : : ||||| : : : : : |||||
386 .....ProLysIleValAlaSnGlnLeuAsnG 394
1134 TTCAACTTGGAGCAGCGCTTACGCGCAAAAG 1162
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
394 hGlnAsnLeuAsnAlaIleAlaIleGln 403
seq_name: /STDLS/gcgdata/geneseq/geneseqp_emb1/AA18786
seq_documentation_block:
ID AA18786 standard; Protein; 509 AA.
XX
AC AA18786;
XX
XX
DE 10-DEC-1997 (first entry)
XX
XX
DE Neisseria adhesion protein (from OrfB).
XX
XX
KM Neisseria gonorrhoea; adhesion; lipoprotein; OrfA; OrfI; OrfB.
XX
XX
OS Neisseria gonorrhoeae.
XX
XX
PN DE19534579-A1.
XX
XX
PD 20-MAR-1997.
XX
XX
PF 18-SEP-1995; 95DE-1034579.
XX
XX
PR 18-SEP-1995; 95DE-1034579.
XX
XX
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX
PI Fischer E, Meier J, Meyer TF, Rudel T, Scheuerpflug I;
XX
XX
DR WPI; 1997-180942/17.
XX
XX
PT Nucleic acids encoding Neisseria adhesion proteins - for therapeutic
PT and diagnostic use
XX
XX
PS Claim 40; Page 11-13; 20pp; German.
XX

```

CC OrfA and OrfB in complexes with the protein PilC are capable of  
 CC adhering to human cells.  
 CC Products obtained from the DNA are useful in medications,  
 CC diagnostic compns. and vaccines, esp. for treatment of  
 CC *Neisseria gonorrhoea* and *N. meningitidis* infections.

XX Sequence 509 AA;

# alignment\_scores:

Quality: 450.00 Length: 417  
 Ratio: 1.875 Gaps: 18  
 Percent Similarity: 57.554 Percent Identity: 32.374

# alignment\_block:

US-09-303-518d-463 x AA18786 ..

Align seg 1/1 to: AA18786 from: 1 to: 509

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31 CTGTCAATCTGGCAGTGTGCGCGCATGCATGCACACGCCATGATT 80
   ::::::::::: ::::: ::::::::::: :::::
16 ILSerLeuLeuGlnIleProIle.....SerHisAlaAsnGlyLe 29
   ::::::::::: ::::::::::: ::::::::::: :::::
81 GGCAGAACGATCCCTTATCCGACAGGTTCTGCACCGTCAGCATTTGCAAC 130
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
29 u.....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluP 44
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
131 CCGACGGGAAATACCACTATTGCGC..AGCAGGGGGAGCTTGCCNAG 177
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
44 roGlyGlyLysTyrHisLeuPheGlyAsnAlaArgLysSerVal..... 58
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
178 CGCAGCGGCATATCGATGTGGAGAACATCAAGACCATCATGTGGGCA 227
   ::::: ::::: ::::: :::::
59 LysAsnArgValLysAlaValGlnThrPheAspAlaThrAlaValGlyP 75
   ::::: ::::: ::::: :::::
228 CCGTATG.....ATTCAACAGCGCGCGCTTGAGAGAAATATGCGCT 268
   ::::: ::::: ::::: :::::
75 oIleLeuProIleThrHisGlnArgThrGlyPheGlnGlyIleIleGlyT 92
   ::::: ::::: ::::: :::::
269 ACATGTCGCCCTTTCCGATCAGCGGACAAATTCATTCGCCCTCGAC 318
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
92 yrgLutThrHisPheSerGlyHisGlnValHisSerProPheAsp 108
   ||| ::::::::::: ::::::::::: ::::::::::: :::::
319 AACCATGCTCATCATCCGATTCGACAGACCGGTAGTCCGTTGACG 368
   ||||| ||| ||| ||||| :::::
109 AsnHisAspSerLysSerThrSerAspPheSerGlyLysValAspGly 125
   ||||| :::::
369 ATTCAAGCCTTTACCGCATTCGAGGAGATAGCAACACCATCCGCG 418
   ||||| :::::
125 yPheThrValTyrGlnLeuHisArgThrGlySerGlnIleHisProAla 142
   ||||| :::::
419 ACGGCTATGACGGGCCACAGGGGGGGGCTATCCCGTCCCAAGGCGG 468
   ||||| :::::
142 spGlyTyrAspGlyProGlnGlyGlyLysTyrProGlnGlyAla 158
   ||||| :::::
469 AGGATATATACAGCTACGACATAAAGGGCTGCCCAATATCCGCT 518
   ||||| :::::
159 ArgAspIleTyrSerTyrHisIleLysGlyThrSerThrLysThrLys 175
   ||||| :::::
519 CAAC.....CTGACCGACAC 555
   ||| :::::
175 eAsnThrValProGlnAlaProPheSerAspArgTyrLeuLysGlnAsn 192
   ||||| :::::
536 GCACGACCGGACAAAGCGCTGCGCAGCGCTTCCACATGCGCGCGATG 585
   ::::::::::: :::::
192 LAGlyAlaAlaSerGlyPheLeuSerArgAlaAspGlnAlaGlyLysLeu 208
   ::::::::::: :::::
586 CTGACGCAAGAGTAGCGCAGCATTCAAACGCGCCACCGCATACAGCCC 635
   ::::::::::: ||| :::::::::::
209 IleTyrPheLysAsnAspProAspLysAsnTyrArgAlaAsnArgMetAsp 224
   ||||| :::::
636 CGAGCTGACGATGGGCAATGCCCGCGCAAGCTTCACAGGACGCTGACG 685
   ||||| :::::

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225 .....AspIleArgGlyIleValGlnGlyAlaValAsn..... 235
686 ATATCGTCAAAAACATCATTCGCGCGGACAGAGAAATTCGCGGCA... 732
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226 .....ProPheLeuThrGlyPheGlnGlyLysGlyValGlyAlaIle 249
   ::::::::::: :::::
733 ...GGCATGCCGTCAGAGGTATAGCGAAGCTCA.....AACAT 770
   ::::::::::: :::::
250 ThrAspSerAlaValSerProValThrTyrAlaAlaAlaArgLysThrLe 266
   ::::::::::: :::::
771 TCGTGTCAATGACAGCGCTTGCGTTCGCTTCCACGAAAACAGATGCGC 820
   ::::::::::: ||| ||| :::::
266 uGlnGlyIleHisAsnLeuGlyAsnLeuSerProGlnValGlnLeuAla 283
   :::::
821 GCATCAACGATTTGGCAGATATGCGG...CAACTCAAAAGACTATGCGCA 867
   ::::: ||| ||| |||
283 lAlaIleSerLeuLeuGlnAspSerAlaPheAlaValLysAspGlyIleAsn 299
868 GCAGCCATCCGCGATTTGGCAGATCCCAAAACCCCAATGCCGCAAGGCAT 917
   ::::: ||||| :::::
300 SerAla...ArgGlnTyrAlaAspAlaHisProAsn..... 311
918 AGAAGCCGTCAGCAATATCTTATGCGACGCCATCCCATCAAGAGATTG 967
   ||| ::::::::::: :::::
311 eThrAlaThrAlaGlnThrAlaLeuAlaValAlaGlnAlaAlaGly... 326
968 GAGCTGTCCGGGAAATACGCGCTTGCGCGCATCAGCGACATCCGTCTC 1017
   ||||| :::::
327 .....ThrValTyrPheLysLysValGlnLeuAs 337
1018 AAGCGGTGCG...AGATGGCGCGCGATTCGATTCGCGAAGGAAATCCGC 1064
   ::::: |||
337 nProThrLysTyrAspTyr..... 343
1065 CGTCAGCGCAATTTTGGCGGATGCGGCAATACCGCATCCGCTT 1114
344 .....ValLysAsnThrGlyTyrGlnLysProAla 353
1115 ACCATTCGCGAATATATCGTTCAAACTTGAAGACGCTTACGCGAAAGAA 1164
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354 AlaArgPro.....MetGlnThrValAspGlyGlnMetAlaGlyLys 367
1165 AACATCACCTCCTCAACCGTGGCGCGCTCAAAACGCAAAAATGTCAAC 1213
   ||::: ||||| :::::
367 sAsnLysProPheLysProSerThrGlnGlnHisSerThrHisSerAsp 383
seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AA136583
seq_documentation_block:
ID AA136583 standard; Protein: 468 AA.
XX
XX AA136583;
XX
AC 08-OCT-1999 (first entry)
XX
DT 08-OCT-1999
XX
DE Neisseria gonorrhoeae antigen encoded by ORF29.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria gonorrhoeae.
XX
PN WO924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.

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396 AlaSerAsnGlyAspTyrHisGlyPheProGlnSerValAspAlaPheSe 412  
1359 TGGGAACGAGATGGAGGTTGATGGAAGCTTATTAATTGACAACTC 1408  
412 T..... 412  
1409 GTGAGCAGGTGAGAAAAATGTTACAGAAACGAAAGAGTACAGT 1458  
412 ..... 412  
1459 AGTCAGTTAAAGCCATGCGCAGACGAAATGGGAAATTAACAGCGTT 1508  
413 ..... GluAsnGlyThrValI 418  
1509 AGATTTAATCATTTATAGTGTGAT.....ATCATAAGAAAGCA 1552  
418 e.....GlnIleValGlyIAspAsnIleValArgHisLysLeuT 432  
1553 CAGTAACAGGAGGCAATGCTTAACCCGTGTGATGTACGGTATACAA 1602  
432 yrlleProGlySerTyrLysGlyLysAspGlyAsnPhgIuTyrIleArg 448  
1603 CAACCTCGGCACCTGATTAACATGGCGTTTAT 1635  
449 GluAlaAspGlyLysIleAsnHisArgLeuPhe 459  
seq\_name: /SIDSL/gcgdata/geneseq/geneseq-embL/AA2000.DAT:AAV74709  
seq\_documentation\_block:  
ID AAV74709 standard: Protein; 385 AA.  
XX  
AC AAV74709;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Neisseria meningitidis ORF 238 protein sequence SEQ ID NO:892.  
XX  
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
KW antibacterial; gene therapy.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9957280-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-US09346.  
XX  
PR 01-MAY-1998; 98US-0083758.  
PR 31-JUL-1998; 98US-0094869.  
PR 02-SEP-1998; 98US-0098994.  
PR 02-SEP-1998; 98US-0099062.  
PR 09-OCT-1998; 98US-0103749.  
PR 09-OCT-1998; 98US-0103794.  
PR 09-OCT-1998; 98US-0103796.  
PR 25-FEB-1999; 99US-0121528.  
XX  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
PI Tettein H, Venter JC;  
XX  
XX WPI: 2000-062150/05.  
DR N-PSDB; AA253471.  
XX  
PT Novel Neisserial polypeptides predicted to be useful antigens for  
XX vaccines and diagnostics  
XX  
XX Claim 2: Page 546; 1453pp; English.  
XX

CC AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941  
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254673 represent  
CC PCR primers used in the exemplification of the present invention. The  
CC polypeptides, the polynucleotides, antibodies and compositions of  
CC the invention can be used as vaccines, as diagnostic reagents, and as  
CC immunogenic compositions. The polypeptides can be used in the  
CC manufacture of medicaments for treating or preventing infection due to  
CC Neisseria bacteria (e.g. meningitis and septicaemia), to detect the  
CC presence of Neisseria bacteria, or to raise antibodies. They may also  
CC be used to screen for agonists or antagonists, which may themselves  
CC have use as antibacterial agents. The polynucleotides of the invention  
XX may also be used in gene therapy protocols.  
XX  
SQ Sequence 385 AA:

alignment\_scores:  
Quality: 408.00 Length: 396  
Ratio: 1.830 Gaps: 17  
Percent Similarity: 56.313 Percent Identity: 31.818

alignment\_block:  
US-09-303-518D-463 x AAV74709 ..

Align seg 1/1 to: AAV74709 from: 1 to: 385

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16 IleSerLeuLeuGlnIleProIle.....SerHisAlaAsnGlyLe 29  
81 GGCAACAGATCCCTTATCCGCGAGGTTCTGACCGTCGACATTTCGAAAC 130  
29 u.....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluP 44  
131 CCGACGGGAATATACCATTCCTGCGC...ACCAGGGGGACCTTCCNAG 177  
44 rGlgLyLysTyrHisLeuPhgIAsnAlaArgGlySerVal..... 58  
178 CGCAGCGGCATATGCGATTGGGAAACATACAAAGCCATGAGTGGGCA 227  
59 LysAsnArgValTyrAlaValGlnThrPheAspAlaThrAlaValGlyPr 75  
228 CCTGATG.....ATTCAACAGCGCGCGCTTGAGAAATATCGGCT 268  
75 oIleLeuProIleThrHisGluArgThrGlyPheGluGlyIleIleGlyT 92  
269 ACATTGTCCGCTTTCCGATCAGCGGACAAATTCATTCGCCCTTGAC 318  
92 yGluThrHisPheSerGlyHisGlyValHisSerProPheasp 108  
319 AACCATGCTCATTCGATTCGATTCAGCAAGCCGTAGTCCGTTGACGG 368  
109 AsnHisAspSerLysSerThrSerAspPheSerGlyGlyValAspGlyL 125  
369 ATTCAAGCCTTACCGCATTCGATTCGAGGATACCAACCATCCCGCG 418  
125 yPheThrValItyrGlnLeuHisArgThrGlySerGluIleHisProGluA 142  
419 ACGGCTATGACGGGCGACAGGCGGCGGCTATCCGCTCCCAAGGCGCG 468  
142 spGlyTyrAspGlyProGlnGlySerAspTyrProProGlyGlyVala 158  
469 AGGATATATACAGCTACGACATAAAGCGTTGCCCAAAATATCCGCT 518  
159 ArgAspIleTyrSerTyrValIySeglyThrSerThrLysThrLysSe 175  
519 CAACGACGACGACAAACGCGACCGGACAAAGCGCTTCGACGCTTC 567  
175 rAsnIleValIProArgAlaPro.....PheSerAspArgIlePL 188  
568 .....CACATCGCGCGCTATGCTGACGCAAGAGTACGCGAGCATTC 612  
.....

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188 eulysgluasnAlaGlyAla.....AlaSerGlyPhe 198
613 .....AACGGCGCACCCGATACAGCCCGCA 638
199 PheSerArgAlaSpGluAlaGlyLysLeuIleTrpGluSerAspProAs 215
639 GCTGGACAGATCGGGCATCGCCGCGAAGCCTTCAACGGCGCATCGAGATA 688
215 nLysAsnTrpTrpAlaAsnArgMetAspArgIleArgGlyIleValGlnG 232
689 TCGTCAAAAAC.....ATCATGGCGCGCGCAGAGAAATTCGCGCGCA 732
232 LysAlaValAsnProPheLeuMetGlyPheGlnGlyIleGlyAla 248
733 .....GGCGATGCCGTGCAGGGTATAGGAGAGCTCAAAATCTGCTGT 776
249 IleThrAspSerAlaValSerProValThrAspThrAlaGlnGlnIle 265
777 CATGCACGGC.....TTGGCTCTGCTTTCACCGCAAAACAGATGG 817
265 rLeuGlnGlyIleAsnHisLeuGlyAsnLeuSerProGluAlaGlnLeu 282
818 CGCGCATCAACGATTTGGCAGATATGGC...CAACTCAAAAGCTATGGC 864
282 LalaAlaThrAlaLeuGlnAspSerAlaPheAlaValLysAspGlyIle 298
865 GCAGCAGCCATCCGATGGATGGAGTCCAAACCCCATTCGCGCAGCAAG 914
299 AsnSerAla...ArgGlnTrpAlaAspAlaHisProAsnIleThrLala 314
915 CATAGAACGGCTGACGCAATATCTTTATGGCAGCCATCCCATCAAGG 963
314 rAlaGlnThrAlaLeuAlaValAlaGlnAlaIleThrValTrpGlyG 331
963 ..... 963
331 LysLysValAlaGluLeuAsnProThrLysTrpAspTrpValLysAsnTr 347
964 .....ATTGAGCTGTCCGGGAAATACGGCTTGGCGGCATCAC 1004
348 GlyTyrLysThrProAlaValArg.....Th 356
1005 GGACATCCCTTCACAGCGGTCCGAGATGGCGCGATCGCATTCGCGAAG 1054
356 rMetHisThrLeuAspGlyLeuMetAlaGlyLysAsnArgPro.... 371
1055 GGAATCCGCGCGTCAGCAGCAATTTGCCGATCGCGCA 1092
372 ..LysSerIleThrSerAsnSerLysAlaAspAlaSer 383

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seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AA1999

seq\_documentation\_block:

ID AAY38582 standard; Protein; 482 AA.

AC AAY38582;

DT 08-OCT-1999 (first entry)

DE Neisseria meningitidis strain A antigen encoded by ORF29.

KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

XX treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.

OS Neisseria meningitidis.

PN W09924578-A2.

PD 20-MAY-1999.

PF 09-OCT-1998; 98WO-1B01665.

PR 01-SEP-1998; 98GB-0019016.

```

PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
PI Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;
XX WPI; 1999-327407/27.
XX N-PSDB; AAZ12045.
DR
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX diagnosis, treatment and prevention of infection
XX
PS Claim 4; Page 145; 524pp; English.
XX
XX Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
XX and N. gonorrhoeae antigenic proteins. They are encoded by open
XX reading frames (ORFs) AAZ11972-212358. The antigenic proteins,
XX their fragments, their nucleic acids and antibodies are used for
XX diagnosis, prevention (as vaccines) or treatment of Neisseria
XX infections, such as meningitis, septicaemia and gonorrhea. Both
XX organisms are closely related. Fragments of the nucleic acids
XX are useful as hybridisation probes and antisense reagents.
SQ
Sequence 482 AA:

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alignment\_scores:  
 Quality: 403.50 Length: 453  
 Ratio: 1.634 Gaps: 21  
 Percent Similarity: 54.525 Percent Identity: 30.243

alignment\_block:

US-09-303-518D-463 x AAY38582 ..

Align seg 1/1 to: AAY38582 from: 1 to: 482

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34 TCACATACGCGAGTGTGCTCCGATGACATGCACACCCCTCAGATTGGC 83
15 AlalleSer**LeuGlnIleProIle...SerHisAlaAsnGlyLeu.. 29
84 AACGATCCCTTTATCCGCGAGTTCGACCCGTCACATTTGCAACCG 133
30 ....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluProG 45
134 ACGGGAATACCACTATTCGCG...AGCAGGGGGAGCTTGCACMACGC 180
45 LysLysTyrHisLeuPheGlyAsnAlaArgGlySerVal.....Lys 59
181 AACGGCCATATCGGATTCGGGAAACATACAAAGCATGATGGCCACCT 230
60 AsnArgValTyrAlaValAlaGlnThrPheAspAlaThrAlaValGlyProI 76
231 GATG.....ATTCACAGCGCGCGGTGAGAGAAATCGGCTACA 271
76 eLeuProIleThrHisGluArgThrGlyPheGlnGlyIleIleGlyLysG 93
272 TTGTCCGCTTTTCGATACGCGGCAAAATTCATTCGCGCTTCGACAC 321
93 LuthrHisPheSerGlyHisGlyHisGlyValHisSerProPheAspAsn 109
322 CATGCTCACATTCGATTCGACGAAGCCGGTATGCCGTTGACGAT 371
110 HisAspSerLysSerThrSerAspPheSerGlyLysValAspGlyLys 126
372 CAGCCTTACCGCATTCGATTCGACGAGATAGCAACACCATTCGCGCAG 421
126 eThrValTyrGlnLeuHisArgThrGlySerGluIleHisProGluAspG 143

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422 GGTATGACGGCGGCAAGGAGGGCGGCTTCCGGCTCCGAAGGCGGAG 477  
 143 LTTTASpSLyProSInGlySerAspTyrPrProPrGInGlyAlaArg 159  
 472 GATATATACAGCTACGACATATAAGCGCGTGGCCCAATAATCCGCTCA 521  
 160 AsPIleTyr\*\*\*\*TjYValLysGlyhnrSerThrLysThrLysSerAs 176  
 522 CCTGACCGCAACACCGCAGCACCGCGCAACGGCTTGGCCGACCGTTTC... 567  
 176 nIleValProAlaPro.....PheSerAspArgTrpLeu 189  
 568 ..CACAAATGCCGGCGCTATGCTGAGCGCAAGGATAGGAGCGAGTAT... 612  
 189 ySgIuAsnAlaGlyAla.....AlaSerGlyPhe 199  
 613 .....AAAGCGCGCACCGGATACAGCCCGGAGCT 641  
 200 SerArgAlaAspGluAlaGlyLysLeuLeuLeuTrpGluSerAspProAsnLys 216  
 642 GGACAGATGGGCAATGCCCGCGAAGCCTTCAACGGCAGCTGACAGATCG 694  
 216 sAsnTrpTrpAlaAsnArgMetAspAspIleArgGlyLysValGInGlyA 233  
 692 TCAAAAC.....ATCATCGCGCGGAGGAGGAATGTGGGGCA... 732  
 233 LaValAsnProPheLeuMetGlyPheGInGlyValGlyLysGlyAlaLe 249  
 733 ...GGCGATCGCGTCAAGGATATAGCAAGAGCTCAACATTCGCTCAT 779  
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 283 LaIleThrAlaLeuInAspSerAlaPheAlaValLysAspGlyIleasn 299  
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 300 SerAla...ArgInTrpAlaAspAlaHisProAsnIleThrAlaThrAl 315  
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 315 aGlnThrAlaLeuAlaValAla\*\*AlaAlaIleThrThrValTrpGly.... 330  
 968 GAGCTGTCCGGGAAA..... 984  
 331 .....GlyLysLysValGluLeuAsnProThrLysTrpAspTrp 343  
 985 .....TAGGGCTGGCGCGCATC..ACGGCAATCCCTGT 1016  
 344 ValLysAsnThrGlyTyr\*\*\*ThrProAlaValArgThrMetHisThrLe 360  
 1017 CAAGCGCTCGCAGATGGCGCGGATGCGATGCGATCCGCAAGGAAATCGCGG 1066  
 360 uAspGlyGluMetAlaGlyLysAsnArgProPro....LysSerIleTr 375  
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 375 hnrSerAsnSerLysAlaAspAlaSerThrGlnProSerLeuGlnAlaGln 391  
 1090 .....GCATACGGCAATATC..... 1104  
 392 LeuIleGlyGluGlnIle\*\*\*\*\*GlyHisAlaTyrAsnLysHisValIle 408  
 1105 ....CCGTCGCCCTTACATTCGCCGAATATCCGTTCAACATTTGGAGAGC 1150  
 408 eaArgGInGInGluPheThrAspLeuAsnIleAsnSerProAlaAspPheA 425  
 1151 GTTACGGCAAGAAACATCACTCTCTACCGTCCGCGCGCTCAACGGCG 12000

```

425  |a|a|g|H|s|I|e|g|I|a|s|H|l|e|v|a|S|e|r|H|i|s|.....P|r|o|*|*|A|s|m|e|t 438
1201 |a|A|A|A|A|T|G|C 1209
439 |l|y|s|G|l|u|e|u 441

```

seq\_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:AAV38581

seq\_documentation\_block:

ID	AAV38581 standard; protein; 483 AA.
XY	

AC AAY38581;

DT 08-OCT-1999 (first entry)

DE *Neisseria meningitidis* antigen encoded by ORF29

KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;

XX

XX 6

XX  
NY 7  
C / C E F C O M

20 OCT 1964  
FEDERAL  
XX

03-001-1550, 50WU-1B01000-  
FE  
XX

PR	01-SEP-1998;	98GB-0019016.
PR	06-NOV-1997;	97GB-0023516

PR	14-NOV-1997;	97GB-0024190.
PR	18-NOV-1997:	97GB-0024196

PR	27-NOV-1997;	97GB-0025158.
ED	10 DEC 1997	07GD 0036147

PR 14-JAN-1998; 98GB-0000759.

PA (CHTR-) CHIRON SPA.

PI Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;

DR WPI; 1999-327407/27.

XX

PT diagnosis, treatment

PS Claim 4; Page 144:

Amino acid sequences AAY38499-Y38944 represent *Neisseria meningitidis*

CC and N. gonorrhoeae antigenic proteins. They are encoded by open  
CC reading frames (ORFs) AA271972-2712358. The antigenic proteins

CC their fragments, their nucleic acids and antibodies are used to  
CC diagnosis prevention (as vaccines) or treatment of *Neisseria*

infections, such as meningitis, septicaemia and gonorrhoea. Both organisms are closely related. Fragments of the nucleic acids

CC are useful as hybridisation probes and antisense reagents.

SQ Sequence 483 AA;

alignment\_scores:

Rat

US-09-303-518D-463 x AAY38581

Align seg 1/1 to: AAY38581 from: 1 to: 483

31 CTGTCATACTGGCAAGTGTGCCCTGCCGATGCATGCACACGCTCAGATT 80

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16 IleSerLeuEngInleProIle.....SerHisAlaasnGlyLe 29
81 GGCAAAAGATCCCTTATCGCGAGGTCTCGACCGTACAGATTGTCGAC 130
29 u.....AspAlaIArgLeuArgAspSerMetGlnAlaLysHisTyrGlu 44
131 CGCAGCGGAATATACACATATTCGGC...AGCAGGGGGAGCTTGGCCMG 177
44 rogluGlyLysTyrHisLeuPheGlyAsnAlaArgLysSerValLysLys 60
178 CGCAACGCCCATATCGGATTGGGAACATACAAAGCCATCAG..... 219
61 Arg.....ValTyrAlaValGlnThrPheAspSerProValThrAl 72
220 .....TTGGGCCACCTGATGATTCACAGAGCGGCGG 250
72 aValSerProValLeuProIleThrHis.....GluArgThrGlyP 86
251 TTGAAGGAATATATCGGCTACATTGTCGGCTTTCCGATCAGGGCAGCA 300
86 hegluGlyValIleGlyTyrGlnThrHisPheSerGlyHisGlyHisGlu 102
301 TTCGATTCCGCTTCGACAAACATGCTCAGATTCCGATTTCAGCAAGC 350
103 ValHisSerProPheAspHisHisAspSerLysSerThrSerAspPhe 119
351 CGGTAGTCCGCTTGAGCGATTACGCTTACCGCATCCGATTCGAGAGGAT 400
119 rGlyGlyValAspGlyGlyPheThrValTyrGlnLeuHisArgThrGlyS 136
401 ACGAACACATCCCGCGCGGCTATGACGGCCAGCGGCGGCGCTAT 450
136 ergluLeuHisProGluAspGlyTyrAspGlyProGlnGlySerAspTyr 152
451 CCGCGTCCCAAGCGCGGAGGATATACAGCTACGACATAAAGCGCT 500
153 ProProGluGlyGlyAlaArgAspIleTyrSerTyrValLysGlyHis 169
501 TGCCCAAAATATCGGCTCAACCTGACCGCACACCGAGACCGGAGCAAC 550
169 rSerThrLysThrLysThrAsnIleValProGlnAlaPro..... 182
551 GCGTTCGCGACCGTTTC.....CACAAATCGCGGCTATGTCGACGCA 594
183 ..PheSerAspArgTyrPleuLysGluAsnAlaGlyAla..... 194
595 GGAGTAGCGCAGGATTC.....AAAGCGCG 620
195 .....AlaSerGlyPhePheSerArgAlaAspGluAlaGlyLysLeuI 209
621 CACCGCATACAGCCGCGAGCTGGACAGATCGGCAATGCGCGGAGGCGT 670
209 eTTPGluSerAspProAsnLysAsnTTPTrpAlaAsnAlaGlyMetAsp 226
671 TCAACGCGACTGCAGATATGTCAAAAC.....ATCATCGCGCGGCA 714
226 alArgGlyIleValGlnGlyAlaValAsnProPheLeuMetGlyPheGln 242
715 GGAGAATTTGTCGGCGCA.....GGCGATGCCGTCGAGGATTAAGCA 758
243 GlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValThr 259
759 AGGCTCAAAATGCTGTCATGCAGCGC.....TTGGGCTGCTTT 799
259 pThrAlaAlaGlnGlnThrLeuGlnGlyLysAsnAspLeuGlyLysLeu 276
800 CCAACGAAACAAAGATGCGCGCATCAACGATTGGCAGTATAGCGC... 846
276 eTTPGluAlaGlnLeuAlaAlaAlaSerLeuEngInAspSerAlaPhe 292
847 CAACCTCAAGACTATGCGCGCAGCGACGATCCGGATTGGCGAGTCCAAA 896
293 AlValLysAspGlyLysAsnSerAla...LysGlnTTPAlaAspAlaH 308

```

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897 CCCCAAT.....GCCGCAAGACATAGAGCGG 925
308 sProAsnIleThrAlaThrAlaGlnThrAlaLeuSerAlaAlaGluAla 324
926 TCAGCAATATCTTTATGCGACGATCCCATCAAAAGGATTGGAGCTGTC 975
325 AlaGly...ThrValTyrArg.....GlyLysLysValGluLeuAs 337
976 CGGGGAAATACGCTTGCGCG.....GCAT 1001
337 nProThrLysTTPAspTTPValLysAsnThrGlyTyrLysLysProAla 354
1002 CAGCGCATCTCTGTCAGCGGTCGACAGATGGCGCGCATTCGATTCGCGA 1051
354 IaArgHisMetGlnThrLeuAspGlyGluMetAla..... 365
1052 AAGGAAATCCGCGCGTCAGCAATTTTGGCGATGCGCATACGCCAA 1101
366 GlyGlyAsnLys.....ProIleLysSerLeuProAs 376
1102 TACG.....CGTCCCTTACCATTCGCGAAATATCCGTCGAA 1139
376 nSerAlaAlaGluLysArgLysGlnAsnPheGluLysPheAsn...SerA 392
1140 CTTCGAGCAGCGTT.....ACGGCAAGAAACATCACCTCTCT 1177
392 sTTPSerSerAlaSerPheAspSerValHisLysThrLeuThrPro 407
seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AAV74708
seq_documentation_block:
ID AAV74708 standard; Protein; 483 AA.
XX
AC AAV74708;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 238 protein sequence SEQ ID NO:890.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99MO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB: AA253470.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics

```





gene therapy; conserved sequence.  
XX  
XX Neisseria sp.  
OS  
XX WO200066741-A2.  
PN  
XX 09-NOV-2000.  
PD  
XX 28-APR-2000; 2000WO-1B00642.  
PF  
XX 30-APR-1999; 99GB-0010168.  
PR  
XX 09-MAR-2000; 2000GB-0005728.  
PR  
XX (CHIR-) CHIRON SPA.  
PA  
XX Rappuoli R;  
PI  
XX WPI; 2000-687543/67.  
DR  
XX Novel Neisserial protein fragments and their corresponding nucleic  
PT acids, useful in the manufacture of medicines for the prevention of  
PT Neisserial infection, and in the manufacture of diagnostic reagents -  
XX  
XX Claim 15; Page 58; 157pp; English.  
PS  
XX The present peptide is a conserved region of a Neisserial protein.  
CC Neisserial proteins containing this sequence, and the nucleic acids  
CC that encode such proteins, are useful in the manufacture of medicines  
CC for the prevention of Neisserial infection, and in the manufacture of  
CC multi-specific diagnostic reagents.  
XX  
SQ Sequence 73 AA;

alignment\_scores:  
Quality: 372.00 Length: 73  
Ratio: 5.239 Gaps: 0  
Percent Similarity: 97.260 Percent Identity: 94.521

alignment\_block:  
US-09-303-518D-463 x AAB37859 ..

Align seg 1/1 to: AAB37859 from: 1 to: 73

1075 AATTTGGCGATGGCGCATACGCCAATATCCCGTCCCTTACCATTCGCG 1124  
|||||  
1 AsnPhenAlaAspAlaAlaTyrAlaTyrProSerProTyrHisSerThr 17  
1125 AATATCCCTTCAACTTGAGCAGCGCTTACGCGCAAGAAACATCACCCT 1174  
|||||  
17 GAsnIleAlaGSerAsnIleuGlnArgTyrGlyGlySerGlnAsnIleThrS 34  
1175 CCTCAACCGTGGCGCGTCAACGGCAAAATGTCAAACTGGCAGACCA 1224  
|||||  
34 eSerThrValProProSerAsnGlyLysAsnValLysIleuAlaAsnLys 50  
1225 CGCCACCCGAGACAGCGGTACCGTTTGACGTAAGGTTTCCGATTT 1274  
|||||  
51 ArgHisProLysThrLysValProPheAspGlyLysGlyPheProAsnPh 67  
1275 TGAGAAAGCAGCTGAATAT 1293  
|||||  
67 eGluLysAspValLysTyr 73

seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: AAB37855

seq\_documentation\_block:

ID AAB37855 standard; Peptide; 63 AA.

AC AAB37855;

DT 26-FEB-2001 (first entry)

XX

DE Neisserial conserved peptide #38.

XX  
XX Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;  
KM gene therapy; conserved sequence.  
XX  
XX Neisseria sp.

PN WO200066741-A2.

XX 09-NOV-2000.

PD 28-APR-2000; 2000WO-1B00642.

PF 30-APR-1999; 99GB-0010168.

PR 09-MAR-2000; 2000GB-0005728.

XX (CHIR-) CHIRON SPA.

PA Rappuoli R;

PI WPI; 2000-687543/67.

DR Novel Neisserial protein fragments and their corresponding nucleic  
XX acids, useful in the manufacture of medicines for the prevention of  
XX Neisserial infection, and in the manufacture of diagnostic reagents -  
XX  
XX Claim 15; Page 58; 157pp; English.

PS The present peptide is a conserved region of a Neisserial protein.

CC Neisserial proteins containing this sequence, and the nucleic acids

CC that encode such proteins, are useful in the manufacture of medicines

CC for the prevention of Neisserial infection, and in the manufacture of

CC multi-specific diagnostic reagents.  
XX  
SQ Sequence 63 AA;

alignment\_scores:  
Quality: 313.00 Length: 63  
Ratio: 5.131 Gaps: 0  
Percent Similarity: 96.825 Percent Identity: 95.238

alignment\_block:  
US-09-303-518D-463 x AAB37855 ..

Align seg 1/1 to: AAB37855 from: 1 to: 63

13 CGCAAAATATCCCTTATTCGTCCATACGTGCGAGTGTGCTGCCGATGCA 62  
|||||  
1 ArgLysIleSerLeuIleLeuSerIleLeuAlaValCysLeuProMetH 17  
63 TGCACAGCCCTCAGATTGGCAACGATCCCTTATTCGCGAGTTCTCG 112  
|||||  
17 sAlaHisIleSerAspLeuAlaAsnAspSerPheIleArgGlnValLeuA 34  
113 ACGTCAGATTCGAACCGGACGCGGAATATACCATTCGCGCAGCAG 162  
|||||  
34 sPargGlnHisPheGlnProAspGlyLysTyrHisLeuPheGlySerArg 50  
163 GGGGAGCTTGCCNAGCGCAACGGCATATCGATTGGGA 201  
|||||  
51 GlyGluLeuAlaGluArgSerGlyHisIleGlyLeuGly 63

seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: AAY38580

seq\_documentation\_block:

ID AAY38580 standard; Protein; 125 AA.

AC AAY38580;

DT 08-OCT-1999 (first entry)

XX

DE Neisseria meningitidis antigen encoded by a partial ORF29.

```

XX  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM  treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
XX
XX  Neisseria meningitidis.
OS
XX  W09924578-A2.
XX
XX  20-MAY-1999.
XX
XX  09-OCT-1998; 98WO-IB0165.
XX
XX  01-SEP-1998; 98GB-0019016.
XX  06-NOV-1997; 97GB-0023516.
XX  14-NOV-1997; 97GB-0024190.
XX  18-NOV-1997; 97GB-0024386.
XX  27-NOV-1997; 97GB-0025158.
XX  10-DEC-1997; 97GB-0026147.
XX  14-JAN-1998; 98GB-0000759.
XX
XX  (CHIR-) CHIRON SPA.
XX
XX  Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;
PI  WPI: 1999-327407/27.
XX  N-PSDB; AA12043.
XX
XX  Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT  diagnosis, treatment and prevention of infection
XX
XX  Claim 4; Page 143; 524pp; English.
XX
XX  Amino acid sequences AA138499-138944 represent Neisseria meningitidis
CC  and N. gonorrhoeae antigenic proteins. They are encoded by open
CC  reading frames (ORFs) AA11972-212358. The antigenic proteins,
CC  their fragments, their nucleic acids and antibodies are used for
CC  diagnosis, prevention (as vaccines) or treatment of Neisseria
CC  infections, such as meningitis, septicaemia and gonorrhea. Both
CC  organisms are closely related. Fragments of the nucleic acids
CC  are useful as hybridisation probes and antisense reagents.
XX
XX  Sequence 125 AA:

```

```

alignment_scores:
  Quality: 264.00      Length: 115
  Ratio: 3.259        Gaps: 1
  Percent Similarity: 70.435      Percent Identity: 45.217

```

alignment\_block:

US-09-303-518D-463 x AAY38580 ..

Align seg 1/1 to: AAY38580 from: 1 to: 125

```

238 CACAGGCGGCGCTTGAAGAAATATCGGCTACATGTGCGCTTTCCGA 287
      ::::::::::: ||||| ||||| :::::::::::
10 GLUARGTHRGlyPheGLuGLyValIleGLyTRGluTRHspHeserGI 26
288 TCAGGCGGCAAAATTCATTCGCGCTTGACACCAATGCCATATCCG 337
      ||||| :::: ||||| ||||| :::: ||| |||
26 YHISGLYHISGLValHISserProHeserPHISspserIysseRT 43
338 ATTCGACGAGCGCGGTAGTCCCGTTGACGATTCAGCGCTTACCGATC 387
      ||||| :::: ||||| :::: ||||| :::: |||||
43 hrseAsPheSerGLyGLyValaspGLyGLyPheThrValTylGLInleu 59
388 CATTGGAGGATACGACACCATCCGCGCGGCTATGACGGGCCACA 437
      ||| ||| ||| ||| ||| ||| ||| ||| |||
60 HIsArgThrTrpserGLuIleHISProGLuAspGLyTrAspGLyProGL 76
438 GGGCGGCGGCTATCCGCTCCCAAGGCGCGGATATATACGCTACG 487
      ||::: ||||| ||| ||||| ||||| ||||| |||||
76 nAlaIaA**TyrProProProGLyGLyAlaArgGLyTyrSerTyrT 93

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488 ACATTAAGCGGTGCCCAATATCGCCCTACACTGACCGACACCGC 537
      ::||| :::: :::: :::: :::: :::: ::::
93 yValIysGLyThrSerThrIysThrIysThrIleValProGLnAla 109
538 AGCACCGGACAGCGCTTGCCGCGCTTCCCAATGCGCGCGCT 582
      ::::: ||| :::: ||||| |||||
110 ProHeserAspArgTrpLeuGLu.....GLuSmaIaGLyAla 122

```

seq\_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: AAB37858

seq\_documentation\_block:

ID AAB37858 standard; Peptide: 41 AA.

AC AAB37858;

DT 26-FEB-2001 (first entry)

DE Neisserial conserved peptide #41.

KM Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

KM gene therapy; conserved sequence.

XX Neisseria sp.

FT Key Location/Qualifiers

FT Misc-difference 23 /label= Val, Ile

PN W0200066741-A2.

PD 09-NOV-2000.

PE 28-APR-2000; 2000WO-IB00642.

PR 30-APR-1999; 99GB-0010168.

PR 09-MAR-2000; 2000GB-0005728.

PA (CHIR-) CHIRON SPA.

PI Rappuoli R;

DR WPI: 2000-687543/67.

PT Novel Neisserial protein fragments and their corresponding nucleic

PT acids, useful in the manufacture of medicines for the prevention of

PS Neisserial infection, and in the manufacture of diagnostic reagents -

Claim 15; Page 58; 157pp; English.

CC The present peptide is a conserved region of a Neisserial protein.

CC Neisserial proteins containing this sequence, and the nucleic acids

CC that encode such proteins, are useful in the manufacture of medicines

CC for the prevention of Neisserial infection, and in the manufacture of

CC multi-specific diagnostic reagents.

Sequence 41 AA:

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alignment_scores:
  Quality: 196.00      Length: 41
  Ratio: 5.026        Gaps: 0
  Percent Similarity: 95.122      Percent Identity: 95.122

```

alignment\_block:

US-09-303-518D-463 x AAB37858 ..

Align seg 1/1 to: AAB37858 from: 1 to: 41

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949 ATCCCATCAAGAGATTGAGCTGTCGCGGAAATATGAGCGCTTGCGCG 998
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 IleProIleIysGLyIleGLyAlaValArgGLyTyrGLyLeuGLyGL 17

```



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869 ....CAGCCATCCGATTTGGCAGTCCAAACCCCAATGCCGACAGG 914
      ||| ||||| ||||| |||||
389 pcysalaprovalaiaile.glyserpro.....AlaArg 400
      ||| ||||| ||||| |||||
915 CATTAAGCCCTGACCAATATCTTTATGAGCCATCCCATCAAGGGA 964
      ||| ||||| ||||| |||||
401 gIyArGArGArGArGArGTrp.....ProArgProGlyGI 412
      ||||| ||||| ||||| |||||
965 TTGAGAGTGT.....CCGGGAATATAGCGTTGGCGGCGATCAG 1005
      ||||| ||||| ||||| |||||
412 yCysSerGysValAlaArgProGlyArgArgArgArgArgArgAlas 429
      ||| ||||| ||||| |||||
1006 GCACATCTCTCAACGCGCTGCAGATGGCGCGATCCGATCGCAAAATAC 1055
      :: ||||| ||||| |||||
429 eArGArGcysArGlyAspGlyAsnThrAlaProTPrCysAlaAlaThr 445
      :: ||||| ||||| |||||
1056 GAAATCCGCGCTGACGCAATTTTGGCGATGGCGCATCCGCAAAATAC 1105
      ::||| ||||| ||||| |||||
446 ArgLeuArGTrpArgArg.....Pr 452
      ::||| ||||| ||||| |||||
1106 CGTCCCTTACCATTCCTCGAATATCGTTCAACTTGGAGCAGCTTA 1154
      ||||| ||||| ||||| |||||
452 oValProArgProAlaAlaGlySerGlyArgAlaGlyAlaSerLeuG 469
      ||||| ||||| ||||| |||||
1155 .....CGCAAGAAAGAACATCCTCTCAACCGTCCGCGCTC 1193
      ||||| ||||| ||||| |||||
469 lnaArgGlyTrpArgArgArgAlaAlaProGlnSerValArgValArgAla 485
      ||||| ||||| ||||| |||||
1194 AAGCGCAAAATGTCAAACTGCGACAGCAACCGCACCCGCAAGACGCG 1243
      ::||| ||||| ||||| |||||
486 AlArGlyArgGlnGlyAlaGlyThrProThrAsnProSerSerArg 502
      ||||| ||||| ||||| |||||
1244 T 1244
      |
502 g 502
```

seq\_name: /STDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:ABG08343

seq\_documentation\_block:

ID ABG08343 standard; Protein; 398 AA.

AC ABG08343;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #8334.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS72530.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

```
XX
PS Claim 20: SEQ ID NO 38702; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 398 AA;
```

#### alignment\_scores:

Quality:	171.50	Length:	443
Ratio:	0.884	Gaps:	26
Percent Similarity:	43.792	Percent Identity:	26.862

#### alignment\_block:

US-09-303-518D-463 x ABG08343 ..

Align seg 1/1 to: ABG08343 from: 1 to: 398

```
15 CAAATATCCCTTATTCCTCATCT.....GGCATGTGCTTGC 55
   ||||| ||| |||||
27 ArgAsnLeuSerArgSerLysHisThrSerProHisSerThrProAl 43
   ||||| ||||| ||||| |||||
56 CGATGCATGCACACGCTCAGATTGGCAACGATCCCTTATCCGGCAG 105
   ||||| ||||| ||||| |||||
43 HisLeuLeuSerLysProProArgSerSerGluValIlyThrHisSerG 60
   ||||| ||||| ||||| |||||
106 GTTTCGACCGTCACCATTTGCAACCGCAGGAAATACCACTATTGCG 155
   ||||| ||||| ||||| |||||
60 lnaValLeuProGlyThrProArg.ProThrSerGlnLeuHisLeuGlu 76
   ||||| ||||| ||||| |||||
156 CAGCAGGGGGGAGCTTGGCCMAGCGCATATCGATTGGGAACA 205
   ||||| ||||| ||||| |||||
76 uValLeuProValPheAlaArgLeuProGlyHisArgGlyIleGluArg 93
   ||||| ||||| ||||| |||||
206 TACAAGCCATCAGTTGGCCACCTGATGATTCAAACAGCGCGCTTGA 255
   ||||| ||||| ||||| |||||
93 lnaGlnSerSerPro..... 97
256 GGAATATTCGCTACATTTGCCGCTTTCGATCAGCGGCAAAATTC 305
   ||||| ||||| ||||| |||||
98 .....TyrSerArgArgGlyHis..... 103
306 TTGCGCCTTGACAACCATGCTCACAATTCGATTTGAGAGACCGGTA 355
   ||||| ||||| ||||| |||||
104 .....HisArgGlyTyrThrGluGluAsp***ValAsn 115
   ||||| ||||| ||||| |||||
115 er*****AspGlyValGluProTyr..... 123
306 GTCCCGTTGACGATTCAGCTTACCGCATTCATGGACGAGTACGAA 405
   ||||| ||||| ||||| |||||
406 CACATCCCGCGCAGGCTATGACGGCCACAG...CGCGCGCGCTATCC 452
   ||||| ||||| ||||| |||||
124 ...GlyLysValAlaAlaAlaGlyProGlnArgGlyArgGlyTyrG 139
```

```

453 CGCTCCCA.....AGGCGAAGGATATATAGACGTACAGCATATAA 495
      ||||| .....||| ||||| |||||
139 scysptotratgatglnlgnlsgl.....Arglnlsatga 152
      ||||| ||||| |||||
496 GGCSTGTCCCAAAATATCCGCT.....CAAGCTGAC 527
      ||||| ||||| |||||
152 rglatg.....ProtrpIlealLeuGlnArgLysGlnProala 164
      ||||| ||||| |||||
528 CGACAAACG.....CACACCGGACAAACGCG 553
      ||| ||| ||| ||| ||| ||| |||
165 ArgThrProSerAlaLargProtrpIleAlaLeuGlnArgLysGlnAla 181
      ||| ||| ||| ||| ||| ||| |||
554 TTGGCGAAGCTTTACAAATGCGCGGCTATGCTGACGAAAGATAGCG 603
      ||| ||| ||| ||| ||| ||| |||
181 aargThrProSerPro.....ArgProtrpIleAlaLeuGlnArg 195
      ||| ||| ||| ||| ||| ||| |||
604 GACGATTCAAACGCGCCACCGCATACAGCCG..... 638
      ||| ||| ||| ||| ||| ||| |||
195 rglAlaArglnlsGlyArglnlsArgProLargProLysArgSerAlaGln 211
      ||| ||| ||| ||| ||| ||| |||
639 .....GCTGACAGATCGCGGACATCGCG 661
      ||| ||| ||| ||| ||| ||| |||
212 LysThrThrAlaArgThrProSerProLargProtrpIleAlaLeuGln 228
      ||| ||| ||| ||| ||| ||| |||
662 CGAAGCTTTCACGCGCATGACATATGCTCAAAACATCATCGCGCG 711
      ||| ||||| ||| ||| ||||| ||| |||
228 gArg.....GlnArglnlsGlyArglnlsArglnlsGlylnlsArgSer 243
      ||| ||| ||| ||| ||| ||| |||
712 CGACGAAATTCGTGCGCGACG.....CGATCGCTGACGAGTAT 752
      ||| ||| ||| ||| ||| ||| |||
243 lAgLysThrThrAlaArgThrProSerProLargProtrpIleAlaLeu 259
      ||| ||| ||| ||| ||| ||| |||
753 AAGCGAAGCTCAAAATGCTGTCAT...CGACGCTTGCGTCTGTT 799
      ||||| ||||| ||| ||| |||||
260 GlnArgLysGlnArglnlsGlyArglnlsArgProLargProtrpIleAla 276
      ||| ||| ||| ||| ||| ||| |||
800 CGACGAAATCAAGATGCGCGGCATCAACGATTTGGACAGATATGCG... 845
      ||||| ||||| ||||| ||||| |||||
276 uGlnArgArg.....GlnArglnlsGlyArglnlsArgPro 288
      ||||| ||||| ||||| ||||| |||||
846 .....GCACTCAAAAGACTGCGCGACGACGACATCGCGATG 884
      ||| ||||| ||||| ||||| |||||
288 rArgProtrpIleAlaLeuGlnArg.....ArgGlnArglnlsGlyArg... 301
      ||| ||||| ||||| ||||| |||||
885 GCGAGTCCAAACCCCAATGCGCGACAAAGCATGAAGCGCTCAAGCAT 934
      ||| ||| .....||| ||||| |||||
302 HisArgProtrpProtrpIleAlaLeuGlnArgLysGlnArg..... 315
      ||| ||| ||||| ||||| ||||| |||||
935 TCGTTATGCGACATCCCATCAAGAGATTTGAGCGTGTCCGGGAAA 984
      ||| ||| ||||| ||||| ||||| |||||
316 .....HisGlyArglnlsArgProtrpProtrpIleAlaLeuG 328
      ||| ||| ||||| ||||| ||||| |||||
985 TACGCTTGCGCGAGT.....CAAGCGCATCTGTCAAGCG 1022
      ||| ||||| ||||| ||||| ||||| |||||
328 lArgThr***ArglnlsArgLysHisArglnlsGly..HisProLysProLe 344
      ||||| ||||| ||||| ||||| ||||| |||||
1023 GTGCGACAGCGCGAGTCCGATTCGCGAAAGGAAATCCCGCGCGAC 1072
      ||||| ||||| ||||| ||||| ||||| |||||
344 u..GlnArgThr***GlnlsGlyCysHisArgLysProtrpProtrpIleAla 360
      ||||| ||||| ||||| ||||| ||||| |||||
1073 ACAATTTTCCGATGCGGACATGACGCAAAATACCCGCTTACCATTC 1122
      ||||| ||||| ||||| ||||| ||||| |||||
361 Leu.....GlnArgThr***ProAlaTrpLrProLysAlaMet... 373
      ||||| ||||| ||||| ||||| ||||| |||||
1123 CGAAATATCCGTTCAAACTTGACAGAGGTTTACGCGAAAGAAACATAC 1172
      ||||| ||||| ||||| ||||| ||||| |||||
374 ....AlaThrHisArgSerThrLysLysIleThrAlaTrpLrProSer 389
      ||||| ||||| ||||| ||||| ||||| |||||
389 rGArgProtrpIleAlaLeuGln 396

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